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-MODEL=frame+ p2n.mode1 - DEV=x1h
-DB=GenEmb1 - OFMT=fastea - SIDFIX=rge - MINMATCH=0.1 - LAODECL=0 - LAODECX=0
-DNITS=bits -START=1 - END=-1 - MATRIX=blosum62 - TRANS=bluman40 . cdi - LIST=45
-DOCALIGN=200 - THR SCORE=pct - THR MAX=100 - THR MIN=0 - ALIGN=15 - MODE=LOCAL
-OUTFWT=pto - NORM=ext - HEAPSIZE=500 - WINLEN=0 - MAXLEN=200000000
-USER=USI0049957 @CGN 1 1 3284 @runat 14052004 100249 1257 - NCPU=6 - ICPU=3
-NO MAAP - LARGEQUERS - NEGG SCORES=0 - WAIT - DESPELOCK=100 - LONGLOG
-DEV TIMEOUT=120 - WARN TIMEOUT=30 - THRADS=1 - SGAPPEY=0 - S - FGAPOP=6
-FGAPEXT=7 - YGAPOP=10 - YGAPEXT=0.5 - DELOP=6 - DELEXT=7
                                                                                                                                                                                                                                                                                                                                    May 16, 2004, 17:52:09; Search time 7695 Seconds (without alignments) 4156.876 Million cell updates/sec
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1 MRGPSGALWLLIALRTVLGG......APLLPLLLPALAARLLPPAL 738
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
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Ygapop 10.0 , Ygapext
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Delop 6.0 , Delext
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29: em vi:*
30: em hvi:*
31: em htg_inv:*
32: em htg_other:*
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37: em htg_vri:*
37: em htg_vri:*
40: em htgo_mus:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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                                            | IleaspThrLeuLysGlyValLysSerCysHisThrGlyIleAsnArgThrValGlyTrp
                                                             421 ATTGACACCCTGAAAGGGGTGAAGTCCTGCCACACGGGCATCAATCGCACAGTGGGCTGG
                                                                                                                       221 AlaGlyAspValAlaPheValLysHisSerThrValLeuGluAsnThrAspGlyLysThr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SerArgAlaAspValThrGluTrpArgGlnCysHisLeuAlaArgValProAlaHisAla
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1. .2368
/ organism="Homo sapiens"
/ organism="Homo sapiens"
/ organism="Homo sapiens"
/ do_xref="taxon:9606"
61. .2277
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/ do_xref="GOA:P08182"
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               28-JAN-1993
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                                                       Mo127.1 GI:14412
melanoma associated protein; p97 melanoma-associated antigen.
Homo sapiens (human)
Homo sapiens (solution)
Homo sapiens (human)
Homo sapiens (hordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 2368)
Brown, J.P., Plowman, G.D., Hellstrom, K.E., Purchio, A.F.,
Pennathur, S., Estin, C.D., Rose, T.M., Hellstrom, I. and Hu, S.L.
Patent: GB 2188637-A 1 07-OCT-1987;
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                 PAT
               2368 bp RNA linear melanoma associated antigen P97
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Mismatches:
Indels:
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H.sapiens mRNA for a
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Best Local Similarity:
Query Match:
DB:
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/mol_type="unassigned DNA"	ent Scores: No.:	<pre>it Similarity: 100.00\$ Conservative: .ocal Similarity: 100.00\$ Mismatches:</pre>	6 Gaps: 7-4 (1-738) x AR084661 (1-2368)	Oy 1 MetArgGlyProSerGlyAlaLeuTrpLeuLeuAlaLeuArgThrValLeuGlyGly 20	Qy . 21 MetGluValArgTrpCysAlaThrSerAspFroGluGlnHisLysCysGlyAsnMetSer 40	Oy 41 GlualapheargGlualaGlyIleGlnProSerLeuLeuCysValargGlyThrSerAla 60	Oy 61 AspHisCysValGlnLeulleAlaAlaGlnGluAlaAspAlaIleThrLeuAspGlyGly 80	Qy 81 AlaileTyrGluAlaGlyLysGluHisGlyLeuLysProValValGluValTyrAsp 100	Qy 101 GlnGluValGlyThrSerTyrTyralaValalaValArgArgSerSerHisValThr 120	Qy 121 IleAspThrLeuLysGlyValLysSerCysHisThrGlyIleAsnArgThrValGlyTrp 140	Oy 141 AsnValProValGlyTyrLeuValGluSerGlyArgLeuSerValMetGlyCysAspVal 160	Oy 161 LeuLysAlaValSerAspTyrPheGlyGlyGlySerCysValProGlyAlaGlyGluThrSer 180	Qy 181 TyrSerGluSerLeuCy8ArgLeuCy8ArgGlyAspSerSerGlyGluGlyValCy8Asp 200	Qy 201 LysSerProLeuGluArgTyrTyrAspTyrSerGlyAlaPheArgCysLeuAlaGluGly 220		241 LeuProSerTrpGlyGlnAlaLeuLeuSerGlnAspPheGluLeuLeuCysArgAspGly	Oy 261 SerArgAlaAspValThrGluTrpArgGlnCysHisLeuAlaArgValProAlaHisAla 280	Db 841 AGCCGGCCCATGTCACCGAGGCAGTGCCATCTGGCCCGGGTGCCTGCTCACGC 900	281 ValValValArgAlaAspThrAspGlyGlyLeuIlePheArgLeuLeuAsnGluGlyGln 3	Db 901 GTGGTGGTCCGGGCCGACACAGATGGGGGGCCTCATCTTCCGGCTGCTCAACGAAGGCCAG 960
Db 1441 AGCTCCCACGCCTTCACCTTGGATGAGCTTCGGGGCAAGCGCTCCTGCCACGCCGGTTTC 1500	481 GlySerProAlaGlyTrpAspValProValGlyAlaLeuileGlnArgGlyPheileArg	Qy 501 ProLygAspCygAspValLeuThrAlaValSerGluPhePheAsnAlaSerCysValPro 520	Qy 521 ValAsnAsnProLysAsnTyrProSerSerLeuCysAlaLeuCysValGlyAspGluGln 540	541 GlyArgAsnLysCysValGlyAsnSerGlnGluArgTyrTyrGlyTyrArgGlyAlaPhe	561 ArgCysLeuValGluAsnAlaGlyAspValAlaPheValArgHisThrThrValPheAsp 	581 AsnThrasnGlyHisAsnserGlubrofrphlaAlaGluLeuArgSerGluAspTyrGlu 1801 AACACAAAGGGCCACAATTCCGAGCCTGGGGCTGAGCTCAAGGTCAAGGAATTGAGGAGGGGGGGG	Oy 601 LeuLeuCysProAsnGlyAlaArgAlaGluValSerGlnPheAlaAlaCysAsnLeuAla 620 Db 1861 CTGCTGTGCCCCAACGGGGCCCCAACGGGTGTCCCAGTTTGCAGCTGCTGCAGTTGCAGTTGCAGCTGCAGTTGCAGCTGCAGTTGCAGTTGCAGCTGCAGTTGCAGTGCTGCAGTTG	621 GlnIleProProHisAlaValMetValArgProAspThrAsnIlePheThrValTyrGly	LeuLeuAspLysAlaGlnAspLeuPheGlyAspAspHisAsnLysAsnGlyPheLysMet 	Argala CGGGCG	681 ValProValGlyGluLysThrThrTyrArgGlyTrpLeuGlyLeuAspTyrValAala	701 LeuGluGlyMetSerSerGlnGlnCysSerGlyAlaAlaAlaProAlaProGlyAlaPro	721 LeuLeuProLeuLeuProAlaLeuAlaArgLeuLeuProProAlaLeu 738	RESULT 2 AR084661	LOCUS AR084661 2368 bp DNA linear PAT 01-SEP-2000 DEFINITION Sequence 1 from patent US 5981194. ACCESSION AR084661. VERSION AR084661.1 GI:10011431	KEYWORDS SOURCE Unknown. ORGANISM Unknown.	REFERENCE 1 (bases 1 to 2368) AUTHORS Jefferies, W.A., McGeer, P.L., Rothenberger, S., Food, M.R., Yamada, T.	and Actualy, 1 TITLE Use of p97 and iron binding proteins as diagnostic and therapeutic agents	JOURNAL Patent: US 5981194-A 1 09-NOV-1999; FEATURES Location/Qualifiers	source 12368 /organism="unknown"

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PI INGEGARUDO HERUSUTOROMU,
PI ANSONII EFU PAACHIO, SHIU ROKU FUU, SURIDOHARU PENNATEYUURU PC
CO7K13/00,A61K39/00,A61K39/12,C12N1/20,C12N5/00,C12N7/04, PC
C12N15/00,
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                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

( Dases 1 to 2368)

Jiyosefu, P.B., Chiyaaruzu, D.I., Guregorii, D.P., Teimoshii, E.R., Karuru, I.H., Ingegarudo, H., Ansonii, E.P., Shiu, R.F. and Suridoharu, P.
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GUREGORII DEI
TTCGACTCCTCCAACTATCATGGCCAAGACCTGCTTTTTCAAGGATGCCACCGTCCGGGCG
                                                 ValproValGlyGluLysThrTyrArgGlyTrpLeuGlyLeuAspTyrValAlaAla
                                                                              2101 GTGCCTGTCGGAGAGAAACCACCTACCGCGGCTGGCTGGGGCTGGACTACGTGGCG
                                                                                                             LeuGluGlyMetSerSerGlnGlnCysSerGlyAlaAlaAlaProAlaProGlyAlaPro
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/product='polypeptide having
melanoma-associated p97
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/product='polypeptide having
melanoma-associated p97
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PN JP 1987294698-A/1
PD 22-DEC-1987
PF 06-FEB-1987 JP 1987026191
PR 07-FEB-1986 US 86 827313, 26-JAN-1987 US JIVOSEFU PII BURAUN, CHIYAARUZU DEI IISUTEIN, PI PUROOMAN,
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PATENT: JP 1987294698-A 1 22-DEC-1987;
ONKOOGEN
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*source: cell_line=SK-MEL28;
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/organism="Homo sapiens"
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topology: Linear;
hypothetical: No;
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B01410.1 G1:2169666
JP 1987294698-A/1.
Homo sapiens (human)
Homo sapiens
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                                                               LysAspLeuLeuPheLysAspSerThrSerGluLeuValPro1leAlaThrGlnThrTyr
                                                                                     1021 AAGGATCTACTCTTCAAAGACTCTACCTCGGAGCTTGTGCCCCATCGCCCACAGACCTAT
                                                                                                                         GluAlaTrpLeuGlyHisGluTyrLeuHisAlaMetLysGlyLeuLeuCysAspProAsn
                                                                                                                                            GAGGCGTGGCCTGGCCTGCATGAGTACCTGCATGAAGGGTCTGCTGTGTGACCCCAAC
                                                                                                                                                                                                          GACATGGCCGTGCCTTCCGCCGGCGCGCCTCAAGCCAGAGATCCAGTGCGTGTCAGCC
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                      961 CGTCTGTTCAGCCACGAGGAGCAGCTTCCAGATGTTCAGCTCTGAGGCCTATGGCCAG
                                                                                                                                                                                          ArgLeuProProTyrLeuArgTrpCysValLeuSerThrProGlu1leGlnLysCysGly
                                                                                                                                                                                                                                                        AspMetAlaValAlaPheArgArgGlnArgLeuLysProGluIleGlnCysValSerAla
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Qy 681 ValProValGluCluLysThrThrTyrArgGlyTrpLeuGlyLeuAspTyrValAlaAla 700 Db 2101 GTGCTGTCGCAGAGAAAACCACTACCGCGGTGGCTGGCTG	2368 bp mRNA linear PAT 2 om patent US 6455494. I:27274554	Unclassing (bases Jefferies and Kennes Use of p9 agents Patent: U	υ c	Alignment Scores: 3.48e-286 Length: 2368 Score: 3936.00 Matches: 738 Score: 100.00\$ Conservative: 0 Best Local Similarity: 100.00\$ Mismatches: 0 Query Match: 6 Gaps: 0	US-10-049-957-4 (1-738) x AR232475 (1-2368) Qy	21 MetGluValArgTrpCysAlaThrSerAspProGluGlnHisLysCysGlyAsnMetSer 	Qy 41 GlualaPheArgGlualaGly1leGlnProSerLeuLeuCysValArgGlyThrSerAla 60 	Qy 61 AspHisCysValGInLeuIleAlaAlaGInGluAlaAspAlaIleThrLeuAspGlyGly 80	Qy 81 AlaileTyrGluAlaGlyLysGluHisGlyLeuLysProValValGlyGluValTyrAsp 100 	Qy 101 GlnGluValGlyThrSerTyrTyrAlaValAlaValValArgArgSerSerHisValThr 120 Db 361 CAAGAGGTCGGTACCTCCTATTACGCCGTGGCTGGGTCAGGAGGAGCTCCCATGTGACC 420	Qy 121 IleaspThrLeuLysGlyValLysSerCysHisThrGlyIleasnArgThrValGlyTrp 140 Db 421 ATTGACACCCTGAAAGGCGTGAAAGTCCTACCACACACCACACAATCGACACAGGCGTGG	

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Query Match: 100.00% Indels: 0 DB: 6 Gaps: 0	-049-957-			181	Qy 61 AspHisCysValGlnLeuIleAlaAlaGlnGluAlaAspAlaIleThrLeuAspGlyGly 80 	Qy 81 AlaileTyrGluAlaGlyLysGluHisGlyLeuLysProValValGlyGluValTyrAsp 100	Oy 101 GlnGluValGlyThrSerTyrTyrAlaValAlaValArgArgSerSerHisValThr 120 	Oy 121 IleAspThrLeuLysGlyValLysSerCysHisThrGlyIleAsnArgThrValGlyTrp 140	Oy 141 AsnValProValGlyTyrLeuValGluSerGlyArgLeuSerValMetGlyCysAepVal 160	Oy 161 LeulysalavalSerAspTyrPheGlyGlySerCysValProGlyAlaGlyGluThrSer 180	Qy 181 TyrSerGluSerLeuCysArgLeuCysArgGlyAspSerSerGlyGluGlyValCysAsp 200	Qy 201 LysSerFroLeuGludrgTyrTyrAspTyrSerGlyAlaPheArgCysLeuAlaGluGly 220	221 AlaGlyAspValAlaPheValLysHisSerThrValLeuGluAsnThrAspGlyLysThr 	Qy 241 LeuBroSerTrpGlyGlnAlaLeuLeuSerGlnAspPheGluLeuLeuCysArgAspGly 260	Qy 261 SerargAlaAspValThrGluTrpArgGlnCysHisLeuAlaArgValProAlaHisAla 280 Db 841 AGCCGGGCCGATGTCACCGAGTGGCAGTGCCATCTGGCCCGGGTGCCTGCTCACGCC 900	Oy 281 ValValArgAlaAspThrAspGlyGlyLeuIlePheArgLeuLeuAsnGluGlyGln 300 	Oy 301 ArgLeuPheSerHisGluGlySerSerPheGlnMetPheSerSerGluAlaTyrGlyGln 320	321 LysaspLeuLeuPheLysaspSerThrSerGluLeuValProllealaThrGlnThrTyr
Db 1561 CCCAAGGACTGTGACGTCGTCACAGCAGCGAGTTCTTCAATGCCAGCTGCGTGCCC 1620		Oy 541 GlyArgAsnLysCysValGlyAsnSerGlnGluArgTyrTyrGlyTyrArgGlyAlaPhe 560 Db 1681 GGCCGCAACAAGACAGCAAGAGAGAGAGATTACGGCGCGCGC		581 ASTITUTE ASSISTANCE STATES	Db 1801 AACACAAACGGCCACAATTCCGAGCCCTGGGCTGTGAGCTCAGGGACTATGAA 1860 Qy 601 LeuLeuCysProAsnGlyAlaArgAlaGluValSerGlnPheAlaAlaCysAsnLeuAla 620	Db 1861 crecretacecechaededeceaagrefrecharrecagecaactreea 1920 Oy 621 Gln1leProProHisalaValMetValArgProAspThrAsn1lePheThrValTyrGly 640	Db 1921 CAGATACCACCCCACGCCCGCACCCCGACACCACCACCTCTATGGA 1980	Db 1981 CTGCTGGACAAGGCCCAGGACCTGTTTGGAGACGACAATAAGAACGGGTTCAAAATG 2040 Qy 661 PheAspSerSerAsnTyxHisGlyGlnAspLeuLeuPheLysAspAlaThrValArgAla 680	Db 2041 Triciacriciacrariarcariaccaadaccriciarriricaadaariaccaccaccacaaca 2100 Qy 681 ValproValGlyGluLysThrThrTrargGlyTrpLeuGlyLeuAspTyrValaala 700	Db 2101 GTGCCTGTCGGAGAAACCACCTACCGGCTGGCTGGGCTG	Db 2161 CTGGAAGGATGTTCTCAGATGTTCTGTTTTTTTTTTTTT	Db 2221 CTGCTCCCGCTGCTGCCCCCCCCCCCCCCCCCCCCCCC	AR364343 LOCUS AR364343 DEFINITION Sequence 1 from patent US 5262177. MUCCESSION AR364343	S inknown. ISM Unknown.	Unclassified. CE 1 (bases) RS Brown, J.P., Estin, C.D., Plowman, G.D., Rose, T.M., Hellstrom, Hellstrom, I., Purchio, A.F., Hu, SL. and Pennathur, S.	TITLE Recombinant viruses encoding the human melanoma-associated antigen JOURNAL Patent: US 5262177-A 116-NOV-1993; FRATURES Location/Qualifiers source 12368	/organism="unknown" /mol_type="genomic DNA" ORIGIN	Alignment Scores: Pred. No.: 3.48e-286 Length: 2368 Score: 335.00 Matches: 738 Percent Similarity: 100.00\$ Conservative: 0 Best Local Similarity: 100.00\$ Mismatches: 0

Qy 481 GlySerProAlaGlyTrpAspValProValGlyAlaLeuileGlnArgGlyPheileArg 500 Db 1501 GGCAGCCTGGAGGTGCCCTGGGGTGCCCTTATTCAGAGAGGCTTCATCCGG 1560 Qy 501 ProLysAspCATGACGTGAGTGCCCTTATTCAGAGAGGCTTCATCCGG 1560 Db 1561 CCCAAGGATGTCCTCACAGCAGTGAGCGAGTTCTTCAATGCCGGCTGCCC 1620 Qy 521 ValAsnAsnProLysAsnTyrProSerSerLeuCysAlaLeuCysValGlyAspGluGln 540 Qy 521 ValAsnAsnProLysAsnTyrProSerSerLeuCysAlaLeuCysValGlyAspGluGln 540 CGTABAARACCCCAACAAACTACCCCCAACAGAGAGAGAGAGAGAGAG	541 GlyArgAsnLysCysValGlyAsnSerGlnGluArgTyrTyrGlyYyrArgGlyAlaPhe	Oy 601 LeuLeuCysProAsnGlyAlaArgAlaGluValSerGlnPheAlaAlaCysAsnLeuAla 620	Qy 661 PheAspSerSerAsnTyrHisGlyGlnAspLeuLeuPheLysAspAlaThrValArgAla 680 [Db 2221 CTGCTCCCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGC	
121 IleAspThrLeuLysGlyValLysSerCysHisThrGlyIleAsnArgThrValGlyTrp 140	S41	LeuproSertrpGlyGlnalaLeuLeuSerGlnAspPheGluLeuLeuCysArgAspGly	01 ArgleuPheSerHisGluGlySerSerPheGlnMetPheSerSerGluAlaTyrGlyGln	36.1 Asphetziorolytelytelytelytelytelytelytelytelytelyte	1321 AGTGGCGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG

241 LeuProSerTrpGlyGlnAlaLeuLeuSerGlnAspPheGluLeuLeuCysArgAspGly 260		361 ArgleuProProTyrLeuArgTrpCysValLeuSerThrProGluileGlniysCysGiy 380	1261 AAGTCCCCCAACAGCAGGGGGATCCAGGCTGAGGCAGGCCGGGGCCTGGGCCCTGGGCCGGGGCCGGGGCCGGGGCCGGGGCCGGGGCCGGGGCCGGGG	1381 CACTATGCCCCGGARGACAGCACCTCGTACTACTGCTGGTGCTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG	ProLygAspCygAspValLeuThrAlaValSerGluPhePheAsnAlaSerCygValPro 	541 GlyArgAsnLysCysValGlyAsnSerGlnGluArgTyrTyrGlyTyrArgGlyAlaPhe 560 1681 GGCCGCAACAAGTGTGGGCAACAGCCAGGAGCGGTATTACGGCTACCGCGGCCCTTC 1740 561 ArgCysLeuValGluAsnAlaGlyAspValAlaPheValArgHisThrThrValPheAsp 580 1741 AGGTGCCTGGTGGAGAATGCGGGTACCCTTCGTCAGGCACACACCGTTTTGAC 1800 581 AsnThrAsnGlyHisAsnSerGluProTrpAlaAlaGluLeuArgSerGluAspTyrGlu 600 1801 AACACAAACGGCCACAATTCCGAGCCTGGGGTCAGGGTCAGGGTCAGAGGACTATGAA 1860
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LIKAVSDYFGGSCVPGAGETSYSESLCRLCRGDSSGESVCDKSPLERYYDYSGAFRCLA
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EAGIOPSLLCVRGTSADHCVQLIAAQEADAITLDGGAIYEAGKEHGLKPVVGEVYDQE
                                                                                               1921 CAGATACCACCCCACGCCGTGATGGTCCGGCCCGACACCAACATCTTCACCGTGTATGGA 1980
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (Bases 1 to 2368)
Rose, T.M., Plowman, G.D., Teplow, D.B., Dreyer, W.J., Hellstrom, K.E. and Brown, J.P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Original source text: Human SK-MEL 28 melanoma cell, cDNA to mRNA, clones p972f1,p971j1 and p9710al.

Draft entry and sequence in computer readable form for [1] kindly provided by T.M.Rose, 29-MAY-1986.

Location/Qualifiers
1. .2368
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Human melanoma-associated antigen p97 (melanotransferrin) mRNA, complete cds.
M12154

M12154.1

Antigen; antigen p97; cell surface glycoprotein; glycoprotein; nelanotransferrin.
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   LeuLeuCysProAsnGlyAlaArgAlaGluValSerGlnPheAlaAlaCysAsnLeuAla
                        GlnIleProProHisAlavalMetValArgProAspThrAsnIlePheThrValTyrGly
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61. .2277
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/codon_start=1
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Qy 581 ASNTHARAGNGLYHISASNSERGLUPROTEDALANIAGIULEUARGSERGLUASDTYRGLU 600 Db 1801 AACACAAGCGCCACAATTCCGAGCCTGGTGGTTGHTHHHHHHHHHH	Qy 701 LeuGluGlyMetSerSerGlnGlnCysSerGlyAlaAlaAlaAlaProAlaProGlyAlaPro Db 2161 CTGGAAGGATGCTCTCAGCAGGGCCCCGGGGCCCCGGGGCCCC Qy 721 LeuLeuProLeuLeuDroAlaLeuAlaAlaArgLeuLeuProProAlaLeu Db 2221 CTGCTCCCGCTGCTGCTGCCGCCCCGCCCGCCCGCCCGC	SOURCE Homo sapiens ORGANISM Homo sapiens Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo. REPERENCE 1 (bases 1 to 2154) AUTHORS Kato, Y., Matsukawa, H., Yoshiwara, Y., Oka, O. and Fujita, T. TITLE Method for determining arthritis related melonotransferrin and a reagent thereof JOURNAL Patent: WO 0111368-1 15-FEB-2001; ORIENTAL YEAST CO LTD, YUKIO KATO, HIROKAZU MATSUKAWA, UTAKA YOSHIWARA, OSAMU OKA, TSUYOSHI FUJITA COMMENT OS Homo sapiens (human) PD 15-FEB-2001 PP 01-FEB-2001 PP 02-MG-2000 WO 2000JP005171 PR 05-AUG-1999 JP 95P 222568	PI YUKIO KATO, HIROKAZU MATSUKAMA, YUTAKA YOSHIWARA, OSAMU OKA, PI TSUYOSHI FUJITA PC GOIN33/574 CC FEATURES FEATURES 1. 2154 CD GOINGING Sapiens" //mol Lype="genomic DNA" //mol Lype="genomic DNA" //db_xref="taxon:9606" Alignment Scores: Pred. No.: 3844.00 Matches: Pred. No.: 3844.00 Matches: Pred. Local Similarity: 100.00\$ Mismatches: Best Local Similarity: 100.00\$
AlaGlyAspValAlaPheValLy8HisSerThrValLeuGluAsnThrAspGlyLysThr GCAGGGGACGTGGAACACACACACGCTACTGGAGAACACGGATGGGAAGACC LeuProSerTrpGlanalaLeuLeuSerGlnAspPheGluLeuLeuCy8ArgAspGly CTTCCTCCTGGGGCCAGGCCTGCTGACACGGATGGT SerArgAlaAspValThrGluTrpArgGlnCy8HisLeuAlaArgValProAlaHisAla	1021 AAGGATCTACTTCAAAGACTCTGCGGAGCTTGTGCCCACACAGACCTAT 1080 341 GlublaTrpLeuGlyHisGluTyrLeuHisAlaMetLySGlyLeuLeuCysAspProAsn 360 1081 GAGGCGTGGCCATGAGTACCTGCACCCATCACACACACCCAAC 1140 361 ArgLeuProProTyrLeuArgTrpCysValLeuSerThrProGluIleGlnLysCySGly 380 1141 CGGCTGCCCCCTACCTGCGCTGGTGTCTCTCCCACTCCCGAGATCTGGA 1200 381 ASpWetAlaValAlaPheArgATGTGTGTCTCTCCCCTCCCGAGATCTGGA 1200 381 ASpWetAlaValAlaPheArgATGTGTGTCTCTCCCCTCCCGAGATCCAGAAGTGTGGA 1200 1201 GACATGGCGTTCGGCCGGCGGCGCTCAAGAGTTCAGCC 1260 401 LysSerProGlHHisCTCGCCGGCAGCGCTCCAGAGTCTCAGTCGTTCAGCC 1260 1261 AAGTCCCCCCAACTGCAGGAGCGGATCCAGGAGCTGAAGGTTTAACA 1320		ProLyshspCyshspValleuThrAlaValSerGluPhePheAsnAlaSerCysValPro

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& £	21 MetGluValArgTrpCysAlaThrSerAspProGluGlnHisLysCysGlyAsnMetSer 40	e 6	381 ABBMECALAYAIAAFMEARGARGAIAKGLEULYSFYOGIULIEGINYBYAISEKALA 400
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8 & 8	GAGGCCTTCCGGGAAGCGGGCATCCAGCCCTCCCTCTGCGTCCGGGGCACCTCCGCC 12 AspHisCysValGlnLeulleAlaAlaGlnGluAlaAspAlaIleThrLeuAspGlyGly 80	SP 63	421 SerGlyGluAspIleTyrThrAlaGlyLysLysTyrGlyLeuValProAlaAlaGlyGlu 440
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a & t	GLGGLUVALGAGGGGGGGGGGGGGGGGGGGGGGGGGGGGG	& 8	461 SerSerHisAlaPheThrLeuAspGluLeuArgGlyLy8ArgSerCy8HisAlaGlyPhe 480
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3 & E	TyrSerGluSerLeuCysArgleuCysArgGlyAspSerSerGlyGluGlyValCysAsp 20 TyrSerGluSerLeuCysArgLeuCysArgGlyAspSerSerGlyGluGlyValCysAsp 20 TyrTriff[[\$ g	541 GlyArgAsnLysCysValGlyAsnSerGlnGluArgTyrTyrGlyTyrArgGlyAlaPhe 560
3 & 5	INSECTION OF THE PROPERTY OF T	\$ g	561 ArgCysLeuvalGluAsnAlaGlyAspvalAlaPhevalArgHisThrThrvalPheAsp 580
3 & 8	AlaGlyAspValAlaPheValLySetThrValLeuGluAsmIhrAspGlyLySThr 24	6 d	581 ASNThrAsnGlyHisAsnSerGluProTrpAlaAlaGluLeuArgSerGluAspTyrGlu 600
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                                                      AACGIGCCTGTGGGCTACCTGGTGGACAGCGGCCGCCTCTCAGTGATGGGCTGTGACGTG
                                                                                                                  CTCAAAGCGGTCAGCGAGTACTTCGGGGGCAGCTGCGTCCCTGGGGCAGGAGACCAGA
                                                                                                                                                             TyrSerGluSerLeuCysArgLeuCysArgGlyAspSerSerGlyGluGlyValCysAsp
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WO 0113951-A/1.

Oryctolagus cuniculus (rabbit)

Cryctolagus cuniculus (rabbit)

Cryctolagus cuniculus (rabbit)

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalla; Eutheria; Lagomorpha; Leporidae; Oryctolagus.

I (bases 1 to 2388)

Kato, Y. and Fujimoto, K.

Chondrogenesis promoter

CHUGAI PHARMACEUTICAL CO LTD, YUKIO KATO, KATSUMI FUJIMOTO

OS Oryctolagus cuniculus (rabbit)

PD 01-3351-A/1

PD 00-13351-A/1

PD 00-13351-A/1

PD 01-3251-A/1

                                                                                  27-AUG-2002
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    /organism="Oryctolagus c/mol_type="genomic DNA"
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Location/Qualifiers
1. 2388 / Arcanism="Oryctolagus cuniculus" / Mol Lype="Benomic DNA" / Mol Lype="Benomic DNA" / Mol Expef="taxon:9986"
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Mismatches:
Indels:
Gaps:
Cl2N15/00
Novel chondrogenesis promoter
Location/Qualifiers
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92.95%
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Novel chondrogenesis promoter.

Novel chondrogenesis promoter.

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Gryctolagus cuniculus (rabbit)

SM Oryctolagus cuniculus

Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.

E I (bases I to 2388).

Kato, Y. and Fulimoto, M.

Novel chondrogenesis promoter

L Patent: JP 200202311-A 3 23-JAN-2002;

JAPAN SCIENCE AND TECHNOLOGY CORP

OS Oryctolagus cuniculus (rabbit)

PN 12 200202311-A/3

PD 23-JAN-2002

PP 07-JUL-2000 JP 2000206566

PI YWIO KATO, KATSUMI FUJIMOTO

PC A61K38/00, A61P19/00, A61P19/02, A61P19/08, CO7K16/18, C12N15/09,

PC C12Q1/68,

PC G12Q1/68,

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GlnileProProHisAlaValMetValArgProAspThrAsnIlePheThrValTyrGly
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AB010995
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/sub_species="Japanese
/db_xref="taxon:9986"
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Oryctolagus cuniculus
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Kawamoto, T.
Direct Submission
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Mkamasu, K., Noshiro, M., Kawashima-Ohya, Y., Fujii, M., Shintani, H.,
Okada, Y. and Kato, Y.
Expression of membrane-bound transferrin-like protein p97 on the
eall surface of chondrocytes
Eur. J. Blochem. 256 (3), 503-509 (1998)
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Mammalia, Eutheria, Lagomorpha, Leporidae, Oryctolagus.
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membrane-bound transferrin-like protein; MTF; melanotransfferin;
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PAHAVVVRADTDAGLI FRLLNEGQRLESHEGSSFQMFSSEAYGQKNLLFKDSTLELVP IATOTYEANLGPEYLHAMKGLLCDPRRLPPYLRWCVLSTPEIQKCGDMAVAFSRQRLK PEIQCVSAESPQHCMEQIQAGHIDAVTLNGEDIHTAGKTYGLIPAGGELYAADDBSNS YFVVAVVKRDSAYAFTVDELRGKRSCHPGFGSPAGWDVPVGALIHWGY RPRNCDVLT AGOPFNASCVPVNNPKKYPSSLCALCVGDEQGRNKCTCNSQRAYGDSGAFKCLVEG AGDVAFVKHTIPPNTGHNEPEPWAHILRSQDYELLCPNGARAEAHGPSGAFKCLNEG HAVWNPPDTNIFTVYGLLBKAQDLFGDDHNKNGFKMFDSSSYHGBLLFKDATTAAVPAVP VGERTTYQDWLGPDYVAALEGWQSQRCSGAAVGAPGSSLLPLLPLAVGLLLSSL"	Length: 2388 Matches: 639 Conservative: 46 Mismatches: 51 Indels: 2 Gaps: 1	(1-2388) (1-2388)	metalguryrtosetyniakeulipueureuneunateungunyaturyrtosetyity 20 	MetGluValArgTrpCysAlaThrSerAspProGluGInHisLysCysGlyAsnMetSer 40 :::	GlublaPheArgGlublaGlyIleGlnProSerLeuLeuCyBValArgGlyThrSerAla 60 :::	AspHisCysValGlnLeulleAlaAlaGlnGluAlaAspAlaIleThrLeuAspGlyGly				ABNValProValGlyTyrLeuValGluSerGlyArgLeuSerValMetGlyCysAspVal 160 		TyrSerGluSerLeuCysArgLeuCysArgGlyAspSerSerGlyGluGlyValCysAsp				CIGCCTCTIGGGGCCACAIGCIGAIGTCACGGGACTTIGAGCIGCIGIGIGCCGGGACGGC 839
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                                                                                                                                                                                       CTGCTGGACAAGGCCCAGGACCTGTTTGGAGACGACCACAACAACAAGAACGGGTTCAAGATG
                                                                                                        PheAspSerSerAsnTyrHisGlyGlnAspLeufeuPheLysAspAlaThrValArgAla
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                                   LeuLeuAspLysAlaGlnAspLeuPheGlyAspAspHisAsnLysAsnGlyPheLysMet
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Location/Qualifiers

1. 4068

/ Organism=Murinae gen. sp./mol_type="unassigned DNA"
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Sequence 1 from Patent W00159459
AX212239
AX212239.1 GI:15524017
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Murinae gen. sp.
Eukaryota; Metazoa; C
Mammalia; Eutheria; R
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Query Match:
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Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K., Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Hsieh, F., Diatchenko, L., Marusina, K., Farmer, A., Rubin, G.M., Hong, L., Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L., Scheetz, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S., Carninci, P., Malek, J., Bonak, S.S., Loquellano, N.A., Peters, G.J., Abramson, R.D., Mallahy, S.J., Bosak, S.A., McEwan, P.J., Malek, J.A., Gunstatne, P.H., Richards, S., Woxley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W., Villalon, D.K., Murny, D.M., Sodesgren, E.J., Lu, X., Gibbs, R.A., Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shevchenko, Y., Bouffard, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D., Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.W., Butterfield, Y. S., Krzywinski, M.I., Skalska, U., Schmutz, J., Myers, R.W., Schnerch, A., Schein, J.E., Jones, S.J. and Marra, M.A. Generation and initial analysis of more than 15,000 full-length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /tissue_type="Mammary tumor. C3(1)-Tag model. Infiltrating ductal carcinoma. 5 month old virgin mouse."
/clone lib="NCI CGAP Mam6"
/lab host="DH10B"
/note="Vector: pCMV-SPORT6"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Series: IRAK Plate: 23 Row: h Column: 19
This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 13994139.

Location/Qualifiers
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Contact: MGC help desk
Email: cgapbs-remail.nih.gov
Tissue Procurement: Jeffrey Green M.D.
Tissue Procurement: Jeffrey Green M.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Baylor College of Medicine Human Genome
Sequencing Center
Center code: BCM-HGSC
Web site: http://www.hgsc.bcm.tmc.edu/cdna/
Contact: amg@bcm.tmc.edu
Gunnarane, P.H., Garcia, A.M., Lu, X., Hulyk, S.W., Loulseged, H.,
Kowis, C.R., Sneed, A.J., Martin, R.G., Muzny, D.M., Nanavati,
A.N., Gibbs, R.A.
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/db_xref="G1:2555674" 
/db_xref="LocusID:30060"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted (27-NOV-2002) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                human and mouse cDNA sequences
Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
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/organiam="Mus musculus"

/mol_type="mRNA"

/strain="FVB\N"

/db_xref="taxon:10090"

/clone="MGC:18315 IMAGE:3672916"
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/db_xref="LocusID:30060"
/db_xref="MGI:1353421"
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Strausberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G.,
Klausner, R.D., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D.,
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Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
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2044 TTTGACTCCTCCAAATATCACAGCCAAGACCTGCTTTTCAAAGATGCTACAGAGCG
                                 SerSerHisAlaPheThrLeuAspGluLeuArgGlyLysArgSerCysHisAlaGlyPhe
                                                             1504 GGCAGCCCAGCGGCGAGGAGGTGCCCATCGGCTCCTCATCCAGCGGGGGTTCATCCGG
                                                                                                                                                                                                                                                                           CCCAAGGACTGTGATGTCCTCACAGCGGTGAGCCAGTTCTTCAATGCCAGCTGCGTCCT
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                                                                                                                                                                                                                                               ProLysAspCysAspValLeuThrAlaValSerGluPhePheAsnAlaSerCysValPro
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                                                                                                                                     481 GlySerProAlaGlyTrpAspValProValGlyAlaLeuIleGlnArgGlyPheIleArg
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        GCCGGTGACGTGGCCTTCGTGAAGCACAGCACAGTGCTGGAAAATACTGATGGAAACACC
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Bukaryota; Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

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Kato, Y. and Fujimoto, K.

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CHUGAI PHARMACEUTICAL CO LTD, YUKIO KATO, KATSUMI FUJIMOTO

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CHUGAI PHARMACEUTICAL CO LTD, YUKIO KATO, KATSUMI FUJIMOTO

OS Mus sp.

CHUGAI PHARMACEUTICAL CO LTD, YUKIO KATO, KATSUMI FUJIMOTO

ON MO 0113951-A/12

PD 01-MAR-2001

PP 21-AUG-2000 WO 2000JP005590

PR 19-AUG-1999 JP 99P 232966

PI YUKIO KATO, KATSUMI FUJIMOTO

PC A61K45/00, A61K38/40, A61K48/00, A61K31/7088, A61K35/32, A61P19/02, PC

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361	ArgleuProProTyrLeuArgTrpCysValLeuSerThrProGluileGlnLysCysGly 380
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1318	LysSerProglnHisCysMetGluArgIleGlnAlaGluGlnValAspAlaValThrLeu 420 :::
421 1378	SerGlyGluAspIleTyrThrAlaGlyLySLySTyrGlyLeuValProAlaAlaGlyGlu 440
441	HisTyralaProGluhspSerSerAsnSerTyrTyrValvalAlavalValArgArgAsp 460
461	SerSerHisAlaPheThrLeuAspGluLeuArgGlyLysArgSerCysHisAlaGlyPhe 480
481 1558	GlyserProAlaGlyTrpAspValProValGlyAlaLeuIleGlnArgGlyPheIleArg 500
501 1618	ProlysaspcysaspvalleuThralavalSerGluPhePheAsnalaSerCysValPro 520
521 1678	ValAsnasnproLysAsnTyrProSerSerLeuCysAlaLeuCysValGlyAspGluGln 540
541 1738	GlyargasniysCysValGlyasnSerGlnGluargTyrTyrGlyTyragGlyalaPhe 560
561 1798	ArgCysLeuValGluAsnalaGlyAspValAlaPheValargHisThrThrValPheAsp 580
581 1858	AsnThrasnGlyHisAsnSerGluProTrpAlaalaGluLeuArgSerGluAspTyrGlu 600
601 1918	LeuleuCysProAsnGlyAlaArgAlaGluValSerGlnPheAlaAlaCysAsnLeuAla 620
621 1978	GINIIEProproHisAlavalMetValArgProAspThrAsnIlePheThrValTyrGly 640
641 2038	Leuleuaspiysaladinaspleuphediyaspasphisasniysasndiyphelysmet 660
661	PheAspSerSerAsnTyrHisGlyGlnAspLeuLeuPheLysAspAlaThrValArgAla 680
681 2158	ValProValGlyGluLySThrThrTyrArgGlyTrpLeuGlyLeuAspTyrValAlaAla 700
701	LeuGluGlyMetSerSerGlnGlnCysSerGlyAlaAlaAlaProAlaProGlyAlaPro 720

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Search completed: May 16, 2004, 22:13:35 Job time : 7793 sec8 Human gen LDLR/TF c LDLR/TF c Human lac Human lac

Sequence

Human lac cDNA enco Human lac Human lac

Gene #304 Human tra Human lac Bovine BG Human lac Human lac Human lac

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Abz82283 P
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Human melanoma-associated antigen p97; Melanotransferrin; GPI; glycosyl-phosphatidylinositol anchor; truncated; soluble; blood-brain barrier; iron binding; Alzheimer's disease; iron metabolism; disorder; haemochromatosis; ischaemic tissue damage; heart disease; skin cancer; brain tumour; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human melanoma-associated antigen p97 coding sequence.
                                                                                                                                                                                                                                                                                                                                                  ALIGNMENTS
                                                                                                                                                                                                     AAQ51346
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AAV43729
ABL65858
ABZ35478
AAQ54229
AAZ56122
AAQ6615
AAD45297
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AAT02999
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         GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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Query Match

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The melanoma-associated antigen p97 has been found to be a GPI-anchored protein expressed on the cell surface which is able to bind iron. A soluble form of p97 can be isolated from the aqueous phase after Triton-X -114 phase separation. The soluble (hydrophilic) form of p74 does not contain ethanolamine and it has a slower rate of transport than GPI-anchored p97. The role of p97 in iron-transport suggests a use in modulating iron uptake by cells; p97, it agonists, antagonists and stimulants may be useful in treatment of conditions where iron-metabolism is disturbed, e.g. haemochromatosis and skin cancer. Expression of p97 and transferrin receptors) by reactive mid-rogilal cells associated with senile plaques in Alzheimer's Disease (AD) provides a means of diagnosing AD. (Updated on 25-MAR-2003 to correct PN field.)
                                                                                                                                                                                                                                    New GPI-anchored and soluble forms of P97 - for treating disorders of iron metabolism, delivering drugs to the brain and for diagnosis and treatment of Alzheimer's disease.
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                                                                                                                             Jefferies WA, Mcgeer PL, Rothenberger S, Food MR, Yamada
                                                                                                                                                                                                                                                                                                                        Disclosure; Page 102-106; 166pp; English.
                                                                                  (UYBR-) UNIV BRITISH COLUMBIA
                                          92US-00912291.
93WO-CA000272
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 201	LysSerProLeuGluArgTyrTyrAspTyrSerGlyAlaPheArgCysLeuAlaGluGly 220
 221	AlaGlyAspValAlaPheValLysHisSerThrValLeuGluAsnThrAspGlyLysThr 240
 241	LeuproSerTrpGlyGlnAlaLeuLeuSerGlnAspPheGluLeuLeuCysArgAspGly 260
 261	SerArgAlaAspValThrGluTrpArgGlnCysHisLeuAlaArgValProAlaHisAla 280
 281	ValValValArgAlaAspThrAspGlyGlyLeuIlePheArgLeuLeuAsnGluGlyGln 300
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321	LysaspleuteuPhelysaspSerThrSerGluLeuValProlleAlaThrGlnThrTyr 340
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 381	ASPMETALAVALALAPHEATGATGGInATGLEULYSPTOGIUIIEGINCYSVALSETALA 400
 401	LysserProginHiscysMetGluhrgileGinAlaGluGinValAspAlaValThrLeu 420
421	SerGlyGluAspIleTyrThrAlaGlyLysLyrGlyLeuValProAlaAlaGlyGlu 440
 441	HisfyrAlaProGluAspSerSerAsnSerTyrTyrValValAlaValValArgArgAsp 460
 461	SerSerHisAlaPheThrLeuAspGluLeuArgGlyLysArgSerCysHisAlaGlyPhe 480
481	GlySerProAlaGlyTrpAspValProValGlyAlaLeuIleGlnArgGlyPheIleArg 500
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This invention relates to chondrogenesis promoters containing a membrane-bound transferrin-like protein (MTf). Chondrogenesis promoters, chondrogenesis regulators, MTf activators, MTf antagonist-containing chondral differentiation inhibitors are useful in diagnosis, prevention and treatment of diseases due to abnormal.chondral metabolism and bone metabolism e.g. bone diseases. The present sequence represents human DNA encoding MTf
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ent of diseases
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Chondrogenesis promoters containing membrane-bound tran protein, useful in diagnosis, prevention and treatment abnormal chondral metabolism and bone metabolism.
                                                                                                                                                                                Disclosure; Page 36-37; 57pp; Japanese
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Cartilage cell differentiation stimulator; osteopathic; Membrane-bound transferrin-like protein; MTf-BP; concanavalin A; ConA; membrane bound type transferrin-like protein; MTf; cartilage disorder; bone metabolism disease; cell differentiation; cell growth; extracellular matrix related disease; gene; ss; human.
                                          CTGCTGTGCCCCAACGGGGCCCGAGCCGAGGTGTCCCAGTTTGCAGCCTGCAACCTGGCA
                                                                                               CAGATACCACCCCACGCCGGATGGTCCCGGCCCGACACCATCTTCACCGTGTATGGA
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/*tag= a
product = "Cell differentiation stimulator associated
protein #4"
                                                                                                                                                   CTGCTGGACAAGGCCCCAGGACCTGTTTGGAGACGACCACAATAAAATG
                                                                                                                                                                                                                                            ValProValGlyGluLysThrTyrArgGlyTrpLeuGlyLeuAspTyrValAlaAla
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                                                                                                                                                                                                                                                                                                              CTGGAAGGGATGTCGTCTCAGCAGTGCTCGGGCGCAGCGGCCCCGGGCGCCCCGGGGCGCCC
                             LeuLeuCysProAsnGlyAlaArgAlaGluValSerGlnPheAlaAlaCysAsnLeuAla
                                                                                 Gln1leProProHisAlaValMetValArgProAspThrAsnIlePheThrValTyrGly
                                                                                                                                    LeuLeuAspLysAlaGlnAspLeuPheGlyAspAspHisAsnLysAsnGlyPheLysMet
                                                                                                                                                                                       PheAspSerSerAsnTyrHisGlyGlnAspLeuLeuPheLysAspAlaThrValArgAla
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A cartilage cell differentiation stimulator useful in the diagnosis biophylaxis, cell differentiation, cell growth and construction of extracellular matrix related diseases.
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                                                                                                                                                                                                                                                                                                                                                 encoding cell differentiation stimulator associated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Disclosure; Page 13-14; 17pp; Japanese
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (KAGA-) KAGAKU GIJUTSU SHINKO JIGYODAN
                                                                                                                                                                                                                                                                                                                                                                                                                                 BP.
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P-PSDB; AAU78363.
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CC The invention describes a cartilage cell differentiation stimulator
CC (containing a membrane-bound transferrin-like protein (MTf-BP) and a
CC membrane bound type transferrin-like protein (MTf) and an animal-derived
CC concanavalin-like drug. The cartilage differentiation stimulator can be
CC used in diagnosis, prevention and treatment of cartilage and bone
CC weed in diagnosis, prevention and treatment of cartilage and bone
CC call differentiation, cell growth and construction of extracellular
CC matrix related diseases. MTf-BP strongly stimulates differentiation of
CC cartilage cells and exhibits similar action mechanism with that of plant
CC derived ConA. This sequence represents a cartilage cell differentiation
CC stimulator associated polypeptide described in the invention

11	X & Z	nce	7	427 A; 766 C;	769 G; 406 T; 0	U; 0 Other;		
	Aligi Pred Score Perce Best Query DB:	ment Scor No.: :: nt Simila Local Sim	ity	0 3936.00 100.00\$ 100.00\$ 6	e	vo m		
MethgglyproSerdlyAlaLeuTrpLeuLeuAhaleuArghrvalleuGlyGly	4	-049-957	4 (1-73	ABK12569				
6. HTGGGGGGTCCGGGGGGTCTGTGGGTGTCTGGGTCTGGCGCGGTGGT	ò	Ħ	MetArgGly	ProSerGlyAlaLe	euTrpLeuLeuLeuAla	LeuArgThrValLeuGlyGly	20	
21 MetGluValArgTrpCysAlaThrSerAspProGluGlnHislysCysGlyAsnMetSer 1121 TrGGAGGTGCCACCTCGAGCCCAGAGCGCCAACTGGGC 121 TrGGAGGTGCGCGCACCTCGGCCCCCAGAGCGCCACACGGGCCACATGGGC 121 TrGGAGGTGCGCGCACCTCGGCCCCCCCCCCCCCCCCCCC	ОЪ	61	ATGCGGGGT	CCGAGCGGGGCTCT	Greerscreer	CTGCGCACCGTGCTCGGAGGC	Ñ	
121 HIGH STATE OF THE PROPERTY	ò	21	MetGluVal	ArgTrpCysAlaT	rSerAspProGluGln	HisLysCysGlyAsnMetSer	40	
41 GlualaPheArgGlualaGlyIleGlnProSerLeuLeuCysValhrgGlyThrSerAla 6 181 GAGGCTTCCGGGACGCTCCCCCCCCCCCCCCCCCCCCCC	QQ	121	ATGGAGGTG	CGGTGGTGCGCCAC	CTCGGACCCAGAGCAG	— (ī)	ω̈	
181 GAGGCCTTCCGGGGCATCCAGCCCTCCTCTCCGGGCGCCCCCCCC	ò	41	GluAlaPhe	ArgGluAlaGlyI]	eGlnProSerLeuLeu	CysValArgGlyThrSerAla	09	
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241 daccarrecorrectedencedencedencedencedencedencedenced	ò	61	SpHisCy	ValGlnLeuIleA]	aAl	>	80	
81 AlaileTyrGluAlaGlyLysGluHisGlyLeulysProValValGlyCluValTyrAsp 1 301 GCCATCTATGGGCCGGAAGCCCCGCTGGTCGGTCGCTGGTCGTTAT 2 301 GCCATCTATGGCCGGAAGCCCCTGAAGCCGGTGGTCGGTC	qq	241	GACCACTGO	GTCCAGCTCATCG	GGCCCAGGAGGCTGAC	GCCATCACTCTGGATGGAGGA	300	•
301 GCRICTATEGRAGE GRANGE GRAN	ò	81	AlaileTyr	GluAlaGlyLysG]	uHisGlyLeuLysPro	ValValGlyGluValTyrAsp	100	
101 GlnGluValGlyThrSerTyrTyrAlavalAlaValArgArgSerSerHisValThr	qa	301	-0			GTGGTGGGCGAAGTGTACGAT	360	
361 Chadded Coccatact The Coccate Coccate Color of the Coccate	ò	101	GlnGluVal	GlyThrSerTyrT	rAlaValAlaValVal	ArgArgSerSerHisValThr	a	
121 IleAspThrLeuLysGlyValLysSerCysHisThrGlyIleAsnArgThrValGlyTrp 421 ATTGACACCTGAAAGGCGTGAAGTCCTGCCACACGGGCATCAATCGCACAGTGGGCTGG 4 ATTGACACCCTGAAAGGCGTGAAGTCCTGCCACACGGGCATCAATCGCACAGTGGGCTGG 4 141 AsnValProValGlyTrLeuValGluSerGlyArgLeuSerValMetGlyCysAspVal 481 AACTGGCCGTGGGGCTGTGTGTGTGTGGGGGGGGCGCCTGCGGTGTGTA 5 161 LeuLysAlaValSerAspTyrPheGlyGlySerCysValProGlyAlaGlyGluThrSer 1 1 1 1 1 1 1 1 1	qq	361	CAAGAGGTC	GGTACCTCCTATT	CGCCGTGGCTGTGGTC	AGGAGGAGCTCCCATGTGACC	~	
421 ATTGACACCTGAAAGGCTGAACCCCCCCCGCGCTCAALCGCAGTGGCCTGG 4 141 AANTGACACCCTGAAAGGCTGAAGTCCCCCCCGGCATCAALTCGCAGCAGTGGCCTGG 4 141 AANTGACACCCGTGAAGCCTGCTGCAGCCCCCTCCGGTCAATGGCCTGCCATGTA 5 161 LeuLysAlaValSerAspTyrPheGlyGlySerCysValProGlyAlaGlyGluThrSer 1 161 LeuLysAlaValSerAspTyrPheGlyGlyGlySerCysValProGlyAlaGlyGluThrSer 1 161 LeuLysAlaValSerAspTyrPheGlyGlyGlySerCysValProGlyAlaGlyGluThrSer 1 161 LeuLysAlaValSerAspTyrPheGlyGlyGlySerCysValProGlyAlaGlyGluThrSer 1 161 LeuLysAlaValSerAspTyrPheGlyGlyGlySerCysCyGcGGGGCGGGGGGCGGGGGGGGGGGGGGGGGGGGG	δ	121	IleAspThr	LeuLysGlyValLy	'sSerCysHisThrGly	IleAsnArgThrValGlyTrp	140	
141 AsnvalProvalGlyTyrLeuValGluSerGlyArgLeuSerValMetGlyCysAsspval	qq	421	ATTGACACC	CTGAAAGGCGTGAA	GTCCTGCCACACGGGC	ATCAATCGCACAGTGGGCTGG	480	
481 AAGGGCCCGGGGCCCCCTCCGGTGGTGTGTATA 161 LeulysAlavalSerAspTyrPheGlyGlySerCysValProGlyAlaGlyGluThrSer 1 161 LeulysAlavalSerAspTyrPheGlyGlySerCysValProGlyAlaGlyGluThrSer 1 161 LeulysAlavalSerAspTyrPheGlyGlySerCysValProGlyAlaGlyGluThrSer 1 181 TyrSerGluSerLeuCysArgLeuCysArgGlyAspSerSerGlyGluGlyValCysAsp 2 181 TyrSerGluSerLeuCysArgLeuCysArgGlyAspSerSerGlyGluGlyValCysAsp 2 181 TyrSerGluSerLeuCysArgLeuCysArgGlyAspSerSerGlyGluGlyValCysAsp 2 182 TyrSerGluSerLeuCysArgLeuCysArgGlyAspSerSerGlyGluGlyValCysAsp 2 201 LysSerProLeuGluArgTyrTyrAspTyrSerGlyAlaPheArgCysLeuAlaGluGly 2 201 LysSerProLeuGluArgTyrTyrAspTyrSerGlyAlaPheArgCysLeuAlaGluGly 2 201 LysSerProLeuGluArgTyrTyrAspTyrSerGlyAlaPheArgCysLeuAlaGluGly 2 201 LysSerProLeuGluArgTyrTyrAspTyrSerGlyAlaPheArgCysLeuAlaGluGly 2 201 LysSerProLeuGluArgTyrTyrAspTyrAspTyrSerGlyAlaPheArgCysCrTGGGGAAGGG 7 201 LysSerProLeuGluArgTyrTyrAspTyrAspTyrSerGlyAlaPheArgCysGaAGGGGGGAAGGGG 7 201 LysSerProLeuGluArgTyrTyrAspTyrAspTyrAspTyrAlleuGluAspThrAspGlyLysThr 7 21 AlaGlyAspValAlaPheValLysHisSerThrValLeuGluAsnThrAspGlyLysThr 7 22 AlaGlyAspValAlaPheValLysHisSerThrValLeuGluAsnThrAspGlyLysThr 7 21 LeuProSerTrpGlyGlnAlaLeuLeuSerGlnAspPheGluLeuLeuCysArgAspSpGly 2	ò	141	SnV 	ValGlyTyrLeuVa	GluSerGlyArgLeu	SerValMetGlyCysAspVal	9	
161 LeuLyshlaValSerAspTyrPheGlyGlySerCysValProGlyAlaGlyGluThrSer 1	qq	481	_8 _8	GTGGGCTACCTGG	GGAGAGCGGCCGCCTC	TCGGTGATGGCTGCGATGTA	540	
541 CTCAAAGCTCTCAGCGACTATTTTGGGGGCAGTCTGCGTCCCGGGGGGGG	ò	191	υ	ValSerAspTyrPh	leGlyGlySerCyBVal	ProGlyAlaGlyGluThrSer	180	
181 TyrSerGluSerLeuCysArgLeuCysArgGlyAspSerSerGlyGluGlyValCysAsp [g	541	CTCAAAGCT	GTCAGCGACTATT	TGGGGCAGCTGCGTC		009	
601 TACTCHGAGTCCCTCTGCCGCGGGGGGGGGGGGGGGGGGG	ò	181	TyrSerGlu	SerLeuCysArgLe	CysArgGlyAspSer	SerGlyGluGlyValCysAsp	200	
201 LysSerProLeuGludArgTyrTyrAspTyrSerGlyAlaPheArgCysLeuAlaGluGly	qq	601	TACTCTGAG	rccrcrerccc	CTGCAGGGGTGACAGC	TCTGGGGAAGGGGTGTGTGAC	099	
661 AAGAGCCCCCTGGAGAGATACTACGACGGGGGCCTTCCGGTGCCTGGCGGGGGGGG	ò		LysSerPro	LeuGluArgTyrTy	rAspTyrSerGlyAla		220	
221 AlaGlyAspValAlaPheValLysHisSerThrValLeuGluAsnThrAspGlyLysThr	q	661	AAGAGCCCC	CTGGAGAGATACTA	CGACTACAGCGGGGCC		720	
721 GCAGGGGACTTTTGTGAAGCACAGCACGTACTGGAAACACACGAAGACA 241 LeuProSerTrpGlyGlnAlaLeuLeuSerGlnAspPheGluLeuLeuCysArgAspGly	ò	221	AlaglyAsp	ValAlaPheValLy	'sHisSerThrValLeu	GluAsnThrAspGlyLysThr	240	
241 LeuProSerTrpGlyGlnAlaLeuLeuSerGlnAspPheGluLeuLeuCysArgAspGly 26	qq	721	GCAGGGGAC	GTGGCTTTTGTGA	GCACAGGACGGTACTG		780	
	ó	241	LeuProSer'	TrpGlyGlnAlaLe	uLeuSerGlnAspPhe		260	

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1 CTTCCCTCCTGGGGCCAGGCCTGTTCAGAGACTTCGAGCTGCTGTGCCGGGATGGT	1 SerArgAlaAspValThrGluTrpArgGlnCysHisLeuA	AGCCGGGCCGATGTCACCGAGTGGGGGGGGGCATCTGGCCCGGGTGCCTGCTCACGC	1 ValvalvalArgAlaAspThrAspGlyGlyLeullePheArg 	1 Ar	 CGTCTGTTCAGCCAGCAGCAGCTTCCAGATGTTCAGCTCTGAGGCCTATGGCCA 	1 LysaspleuLeuPheLysaspSerThrSerGluLeuValPro	1 GluAlaTrpLeuGlyHisGluTyrLeuHisAlaMetLysGlyLeuLeuCysAspProAs			1 CGGCTGCCCCCTACCTGCTGGTGTGCTCTCCCACTCCCGAGATCCAGAAGTGTGG	1 AspMetAlaValAlaPheArgArgGlnArgLeuLyaProGlulleGlnCysValSerAla	1 LysSerProGlnHisCysMetGluArglleGlnAlaGluGlnValAspAlaValThrLe		1 SerGlyGluAspileTyrThrAlaGlyLysLysTyrGlyLeuValProAlaAlaGlyGl		1 HisTyrAlaProGluAspSerSerAsnSerTyrTyrValValAlaValArgArgAsp	1 cactatécecedaadacadeadeactecatactacordesceceregadacesea	1 SerSerHishlaPheThrLeuAspGluLeuArgGlyLyshrgSerCysHisAlaGlyPhe	lySerProAlaGlyTrpAspValProValGlyAlaLeuIleGlnArqGlyPheIleAr		1 ProLysAspCysAspValLeuThrAlaValSerGluPhePheAsnAlaSerCysValPro	CCAAGGACTGTGTCTCTCACAGCGAGTTGTTTCTATGCCAGCTGCGTGCC	1 ValAsnAsnProLysAsnTyrProSerSerLeuCysAlaLeuCysValGlyAspGluGln	GTGAACAACCCCAAGAACTACCCCTCCTGTGTGCACTGTGCGGGGGGGACGAGCA	1 GlyArgAsnLysCysValGlyAsnSerGlnGluArgTyrTyrGlyTyrArgGlyAlaPhe	ccgcaacaagtgtggggaacagccaggagggggtattacggctaccgcgcgcctt	1 ArgCysLeuValGluAsnAlaGlyAspValAlaPheValArgHisThrValPheAsp	gitacaitadada a da	1 AsnThrasnGlyHisAsnSerGluProTrpAlaAlaGluLeuArgSerGluAspTyrGlu	CACAAACGGCCACAATTCCGAGCCCTGGGCTGAGGTCAGGTCAGAGGACTATGA	1 LeuLeuCysProAsnGlyAlaArgAlaGluValSerGlnPheAlaAlaCysAsnLeuAla
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melanoma. Insertion of the p97 gene into vaccinia virus yields the recombinant virus Vp97a-NY. BSC cells infected with this virus produce large amts. of p97, and the virus has immunogenic activity in vivo. (Updated on 01-JUL-2002 to add missing PI field.) (Updated on 25-MAR-2003 to correct PA field.)
                                                                                                                                                                                                                                                                                     AlaileTyrGluAlaGlyLysGluHisGlyLeuLysProValValGlyGluValTyrAsp 100
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                 | GlnIleProProHisAlaValMetValArgProAspThrAsnIlePheThrValTyrGly
                                CAGATACCACCCCACGCCGTGATGGTCCGGCCCGACACACATCTTCACCGTGTATGGA
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The present invention relates to a method for the diagnosis of arthritic disorders, by assay of melanotransferrin in a biological sample, and deducing the presence of an arthritic disorder from the presence of a concentration of melanotransferrin significantly higher than in non-arthritic subjects. The method can be used for the diagnosis of arthritic disorders including rheumatoid arthritis, osteoarthritis and joint trauma. The present sequence is the coding sequence for human MTF, which was used in the present invention
                                                                                                                                                                                                                                                                                                                       Human; MTF; arthritic disorder; melanotransferrin; rheumatoid arthritis; osteoarthritis; joint trauma; ss.
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LeuLeuAspLysAlaGlnAspLeuPheGlyAspAspHisAsnLysAsnGlyPheLysMet
                                                                                                                                                                    Assay of melanotransferrin by sandwich immunoassay in blood fluid for diagnosis of arthritic disorders.
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ý f	41 GlualapheargGlualaGly1leGlnProSerLeuLeuCysValargGlyThrSerala 60	දුරු දුර	401 LysSerProGlnHisCysMetGluArgileGlnAlaGluGlnValAspi
8 8 8	AspHisCysValGlnLeulleAlaAlaGlnGluAlaAspAlaIleThrLeuAspGlyGly 8	& 8	421 SerGlyGluAspIleTyrThrAlaGlyLysLysTyrGlyLeuValProi
දී රි සි	121 GACCACTGCGTCCAGCTCATCGCGGCCCCAGGAGGCTGACGCCATCACTCTCGGAGGGA 180 81 Ala1leTyrGluAlaGlyLysGluHisGlyLeuLysProValValGlyGluValTyrAsp 100 111	oy Oy	441 HistyrAlaProGluAspSerSerAsnSerTyrTyrValValAlaVal'
3 8 8	GinGluValGlyThrSerTyrTyrAlaValAlaValArgArgSerSerSerHisValThr 	දු පු	461 SerSerHisAlaPheThrLeuAspGluLeuArgGlyLysArgSerCysl
3 8 8	IleAspThrLeuLysGlyValLysSerCysHisThrGlyIleAsnArgThrValGlYTrp 	\$ A	481 GlySerProAlaGlyTrpAspValProValGlyAlaLeuIleGlnArg(
3 & i	AsnValProValG1yTyrLeuValG1uSerG1yArgLeuSerValMetG1yCysAspVal	දු පු	501 ProLysAspCysAspValLeuThrAlaValSerGluPhePheAsnAlatel
8 & 1	361 AACGIGGCCCGIGGGCTACCTGGIGGAGGGGCCCCCTCTCGGIGATGGGCTGCGATGTA 420 161 LeuLysAlaValSerAspTyrPheGlyGlySerCysValProGlyAlaGlyGluThrSer 180	ob ob	521 ValasnAsnProLysasnTyrProSerSerLeuCysAlaLeuCysVal(
g & :	TyrSerGluSerLeuCysArgLeuCysArgGlyAspSerSerGlyGluGlyValCysAsp 2	ò a	541 GlyargAsnLysCysValGlyasnSerGlnGluargTyrTyrGlyTyr
දී හි ර	TACTCTGAGTCCCTCTGTCGCCTCTGCAGGGGTGACAGCTCTGGGGAAGGGGTGTGTGAC LysSerProLeuGluArgTyrTyrAspTyrSerG1yAlaPheArgCysLeuAlaGluG1y 	& 8	561 ArgCysLeuValGluAsnAlaGlyAspValAlaPheValArgHisThr'
8 8 8	Asassccccccissasariaciacsaciacsassccriccssisscrissssssssss	ò a	581 AENThrAsnGlyHisAsnSerGlubroTrpAlaAlaGluLeuhrgSer(
8 & 6	501 GCAGGGACGACGAGGACACACACACGGAGGAGAGAACACGGAGAGACGGAGGA	oy d	601 LeuleuCysProAsnGlyAlaArgAlaGluValSerGlnPheAlaAla
કે જે કે	SerArgAlaAspValThrGluTrpArgGlnCysHisLeuAlaArgValProAlaHisAla	oy G	621 GlnileProProHisAlaValMetValArgProAspThrAsnilePhe'
g & 1	.Accossociosatsicaciosasisoassocasisociaticassociaticacios as valvalvalvalargalaaspihraspglyGlyGlyEeullePheArgLeuLeuAsnGluGlyGln 30	oy O	641 LeuleuAspLysAlaGlnAspLeuPheGlyAspAspHisAsnLy
8 & 1	781 GTGGTGGTCCGGGCCGACACAGATGGGGGCCCTCATCTTCCGGCTGCTCAAGGGCCAG 840 301 ArgleupheSerHisGluGlySerSerPheGlnMetPheSerSerGluAlaTyrGlyGln 320	∂ ଶ୍	661 PheaspSerSerAsnTyrHisGlyGlnaspLeuLeuPheLysAspAla'
3 8 8	LysaspleuLeuPheLysaspSerThrSerGluLeuValProIleAlaThrGlnThrTyr 	\$ 8	681 ValProValGlyGluLysThrThrTyrArgGlyTrpLeuGlyLeuAsp'
3 8 8	GlualaTrpLeuGlyHisGluTyrLeuHisAlaMetLysGlyLeuLeuCysAspProAsn 360	oy G	701 LeuGluGlyMetSerSerGlnGlnCysSerGlyAlaAlaAlaProAla!
8 & ,	961 GAGGCGIGGCCCATGAGIACTGCACGCCATGAGGCGTCTGCTCTGTGACCCCAAC 1020 361 ArgLeuproProTyrLeuArgTrpCysValLeuSerThrProGluIleGlnLysCysGly 380 [oko qa	721 LeufeuProfeuLeufeuProAlafeuAlaArgfeufeuProPro 11

erGluaspTyrGlu 600 |||||||||||||| |AGAGGACTATGAA 1740 | Incompage | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 roalaalagiygiu 440 |||||||||||||||| |cgcagccgccag 1260 aCysAsnLeuAla 620 |||||||||||||| |CrGCAACCTGGCA 1800 snGlyPheLysMet 660 |||||||||||||| |ACGGGTTCAAAATG 1920 laProGlyAlaPro 720 CCAGAAGTGTGGA 1080 1Valargargasp 460 'sHisAlaGlyPhe 480 aSerCysValPro 520 /rargGlyAlaPhe 560 |||||||||||||| \ccGcGcGccTTC 1620 roAlaLeu 738 ||||||||| |CGCCCTC 2154

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                         GCCATTTACGAGGCGGGAAGGAACACGGCCTGAAGCCCGTGGTGGCGCGAAGTGTATGAC
                                                GlnGluValGlyThrSerTyrTyrAlaValAlaValValArgArgSerSerHisValThr
                                                                                                   IleAspThrLeuLysGlyValLysSerCysHisThrGlyIleAsnArgThrValGlyTrp
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This invention relates to chondrogenesis promoters containing a membrane bound transferrin-like protein (MTf). Chondrogenesis promoters, chondrogenesis regulators, MTf activators, MTf antagonist-containing chondral differentiation inhibitors are useful in diagnosis, prevention and treatment of diseases due to abnormal chondral metabolism and bone metabolism e.g. bone diseases. The present sequence represents rabbit DN
                                                                                                                                                                                                                                                                                                                                                                                                    Chondrogenesis promoters containing membrane-bound transferrin-like protein, useful in diagnosis, prevention and treatment of diseases due abnormal chondral metabolism and bone metabolism.
                                                                                                                          Chondrogenesis promoter; membrane-bound transferrin-like protein; MTf; Chondrogenesis regulator; MTf activator; bone metabolism; rabbit; chondral differentiation inhibitor; bone disease; ds.
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Membrane-bound transferrin-like protein; MTf-BP; concanavalin A; ConA;
membrane bound type transferrin-like protein; MTf; cartilage disorder;
          1500 GGCAGCCGGCCGGCTGGGACGTCCCGGTGGGCGCCCTCATCCACTGGGGCTACATCCGG
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441 HisTyrAlaProGluAspSerSerAsnSerTyrTyrValValAlaValValArgArgAsp
                                         SerSerHisAlaPheThrLeuAspGluLeuArgGlyLysArgSerCysHisAlaGlyPhe
                                                                                 GlySerProAlaGlyTrpAspValProValGlyAlaLeuIleGlnArgGlyPheIleArg
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(containing a membrane-bound transferrin-like protein (Wrf-BP) and a membrane bound type transferrin-like protein (Mrf)) and an animal-derived concanavalin-like drug. The cartilage differentiation stimulator can be used in diagnosis, prevention and treatment of cartilage and bone metabolism diseases. They can also be used for diagnosing biophylaxis, cell differentiation, cell growth and construction of extracellular matrix related diseases. Mrf-BP strongly stimulates differentiation of cartilage cells and exhibits similar action mechanism with that of plant derived ConA. This sequence represents a cartilage cell differentiation stimulator associated polypeptide described in the invention
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      invention describes a cartilage cell differentiation stimulator
bone metabolism disease; cell differentiation; cell growth; extracellular matrix related disease; gene; ss; rabbit.
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Mouse; mp97 protein; scialoglycoprotein; neuroprotective; antibacterial; analgesic; nootropic; cytostatic; neuroleptic; virucide; anticonvulsant; deficiency disease; Wernicke's disease; neurodegenerative disease; pain; mutritional polyneuropathy; neurological disorder; cancer; gene therapy; Huntington's disease; Alzheimer's disease; Parkinson's disease; epilepsy; demyelinating disease; multiple sclerosis; amyotrophic lateral sclerosis;
                                                       ProLysAspCysAspValLeuThrAlaValSerGluPhePheAsnAlaSerCysValPro
                          GlySerProhlaGlyTrpAspValProValGlyAlaLeuIleGlnArgGlyPheIleArg
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The invention relates to mouse p97 protein, mp97 (a scialoglycoprotein) and its corresponding cDNA molecule. Mouse p97 protein and its DNA molecule are useful for identifying compounds that affects mp97 protein activity or expression. The invention also relates to a method for conditions, such as cancer, neurodegenerative diseases (e.g., Alzheimer's disease, Parkinson's disease, Huntington's disease), demyelinating diseases (e.g., multiple sclerosis), amyotrophic lateral sclerosis, disease, untrilla ind viral infections, deficiency diseases (e.g., wennicke's disease, nutritional polyneuropathy), epilepsy, psychosis, pain and neurological disorders, especially Alzheimer's disease. Mouse p97 DNA's

Claim 25; Page 53-54; 70pp; English.

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are also useful in gene therapy. Mp97 proteins are useful for delivering therapeutic agents and pharmaceuticals across the blood placenta barrier as well as to other organs including liver. The invention is also useful for preparing antibodies and antisense oligonuclectides, the preparation of experimental systems to study mp97, and in diagnostic and therapeutic applications. Transgenic p97 mice is useful for identifying essential physiological roles for p97 in development and adult functioning of the organism and for testing potential therapeutic and diagnostic agents that are conjugated to p97 protein. The present cDNA sequence encodes mouse p97 (mp97) protein
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Chondrogenesis regulator; MTf activator; bone metabolism; mouse;
chondral differentiation inhibitor; bone disease; ds.
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                                                                          720
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New anticoagulant protein, draculin, from vampire bat saliva - and related nucleic acid, vectors, transformed cells and probes, for treating myocardial infarction, etc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Anticoagulant; Draculin; saliva; vampire bat; inhibition; factor IX; factor X; blood coagulation cascade; serine protease inhibitor; PMFS; acute mycardial infarction; deep vein thrombosis; pulmonary embolism; unstable angina; transient ischemic attack; peripheral vascular; DFP; bypass occlusion; disseminated intravascular coagluation; ds.
LeuGluGlyMetSerSerGlnGlnCysSerGlyAlaAlaAlaProAlaProGlyAlaPro
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P-PSDB; AAR71037.
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                                                                                                                                                                                                                                                           RESULT 10
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                                                                                                                                                                    2098 CTGGAAGCCTGTACCTTCCTGAGGAATTGAAACCAAGAAGGTGGCCCCAGCCCCTGCCAC
                                                      695 LeuAspTyrValAlaAlaLeuGluGlyMetSerSerGlnGlnCysSerGlyAla----
                                                                             2044 CCAGAGTATGTCACAGCGGTTGCTAATCTG-----AGGCAATGCTCCACCTCCCCACTT
                                                                                                                                  ProbeuleuProleuLeuProAlaLeuAlaAlaAlaArgLeuLeuProProAla 737
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 2327 BP; 624 A; 535 C; 629 G; 539 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PA field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DNA encoding human transferrin - used for recombinant amts. of human transferrin for use in tissue culture.
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US-10-049-957-4 (1-738) x AAQ12152 (1-2327)	Oy 1 MetArgGlyProSerGlyAlaLeuTrpLeuLeuLeuAlaLeuArgThrValLeu 18	GlyGlyMetGluValArgTrpCysAlaThrSerAspProGluGlnHisLysCysGlyAsn	Oy 39 MetSerGlualaPheArgGluAlaGlyIleGlnProSerieu 52	LeuCysValArgGlyThrSerAlaAspHisCysValGlnLeuIleAlaAlaGlnGluAla	AspalarleThrLeuAspGlyGlyAlarleTyrGluAlaGlyLysGluHisGlyLeu	259 GANGCIGIGACACIGGAIGCAGGITIGGIGIAIGAIGCITACITGGCICCCAAIAACCIG 318 92 LysProValValGlyGluValTyrAspGlnGluValGlyThrSerTyrTyrAla 109 119 AAGCCIGIGGIGGCAAAGTTCRAAGGAICATCAAAAGAACGAACTTACTATAATAAGT 178	ValalaValValArgArgSerSerHisValThrIleAspThrLeuLysGlyValLysSer 	130 CysHisThrGlylleAsnArgThrValGlyTrpAsnValGlyTyrLeuValGlyTyrLeuValGlu 149	SerGlyArgLeuSerValMetGlyCygAspValLeuLys 16	AlaValSerAspTyrPheGlyGlySerCysValProGlyAlaGlyGluThrSerTyrSer 	GluSerLeuCysArgLeuCysArgGlyAspSerSerGlyGluGlyValCysAspLysSer	ProLeuGluArgTyrTyrAspTyrSerGlyAlaPheArgCysLeuAlaGluGlyAlaGly Archivactaarcaaracaracarcacaagcmicaaaaaaaaaaaaaaaaaaaaaaaaaaaaaa	AspValAlaPhevalLySHisSerThrValLeuGluAsnThrAspGlyLySThrLeuPro	243 SerTrpGlyGlnAlaLeuLeuSerGlnAspPheGluLeuLeuCysArgAspGlySer 261 242	ArgalaaspValThrGluTrpArgGlnCysHisLeuAlaargValProAlaHisAlaVal	ValValArgAlaAspThrAspGlyGlyLeuIlePheArgLeuLeuAsnGlu	GlyGlnArgLeuPheSerHisGluGlySerSerPheGlnMetPheSerSerGluAla	TyrGlyGlnLygAspLeuLeuPheLygAspSerThrSerGluLeuValProIleAlaThr:::

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The present sequence is that of a nucleic acid encoding human transferrin (Tf). The invention relates to modified Tf fusion proteins comprising at least one therapeutic protein, polypeptide or peptide, in which the Tf portion is engineered to extend the serum half-life or bioavailability of the molecule. The modified Tf fusion protein preferably comprises a human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New fusion protein, useful in the diagnosis and treatment of diseases or disorders relating to the respiratory, cardiovascular and digestive systems, comprises a transferrin protein fused to a therapeutic protein.
                                                       2056 AAGGCTGTTGGTAACCTG----AGAAAATGCTCCAACTCATCA-----
679 ArgAlaValProValGlyGluLysThrThrTyrArgGlyTrpLeuGlyLeuAspTyrVal
                                          699 AlaAlaLeuGluGlyMetSerSerGlnGlnCysSerGlyAlaAlaAlaProAlaProGly
                                                                                    719 AlaProLeuLeuProLeuLeu-LeuProAlaLeuAlaAlaArgLeu
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                                                                                                                                                                                                                                                           Human transferrin coding sequence
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                                                                                                                                                                                             ABZ82283 standard; cDNA; 2318
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2001US-0334059P.
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P-PSDB; ABP72819.
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Tf moiety that has been modified to reduce or prevent glycosylation, iron binding and/or transferrin receptor binding. Nucleic acids encoding such fusion proteins, vectors, host cells and transgenic animals which produce the fusion protein in their serum or milk are also claimed. The modified fusion protein is useful for treating a disease or disease symptom, or for delivering a therapeutic agent complexed to the ferric iron of transferrin to the inside of a cell or across the blood-brain barrier. The modified fusion protein, or a nucleic acid encoding it, can be used in the diagnosis, prognosis, prevention and/or treatment of diseases and/or alsorders of the endocrine, nervous, immune, respiratory, cardiovascular, reproductive and diseasive systems, diseases and/or disorders relating to the blood or to cell proliferation, inflammatory conditions, and to treat viral, fungal, bacterial or parasitic infection
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This invention describes novel recombinant human serum transferrin mutants with altered metal binding properties. The products of the invention act as iron chelators. The recombinant transferrins can be used in metal chelation therapy to bind and clear excess toxic metals in patients suffering from metal overloads. In particular transferrin mutants which bind iron with higher avidity than natural transferrin can be administered to individuals suffering from thalassemia to remove excess toxic iron from the body. Half-molecules or transferrin mutants with altered metal ion selectivities could be used to clear other toxic metals e.g. lead, mercury, cadmium copper or zinc from the body. Recombinant full length transferrin can also be used in non serum supplements or in tissue culture media. A transferrin half-molecule is and can be excreted in the urine, unlike the holo-proteins, so that the metal is not only chelated but also cleared from the body. The single half-molecules do not bind to transferrin receptors on the membrane of tissue cells and therefore do not deliver the iron to these tissues. A further advantage is that the human body probably recognizes the half-molecules as 'self' and would not elicit an immunological response. Using recombinant transferrin avoids the risk of contamination with HIV or metal is virus associated with transferrin purified from human serum.
                                                                                                                                                                                            Recombinant human serum transferrin mutants with altered metal binding properties are useful in metal chelation therapy and to clear excess toxic metals in patients.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          sequence encodes the human serum transferrin described in the
                                                                           Mason AB;
UNIV VERMONT & STATE AGRIC COLLEGE UNIV BRITISH COLUMBIA.
                                                                         Woodworth RC,
                                                                                                                                                                                                                                                                                          Disclosure; Col 19-24; 26pp; English.
                                                                         Macgillivray RTA,
                                                                                                                      WPI; 2000-022329/02
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  (UYVE-)
                         (UYBR-)
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Sequence 2327 BP; 623 A; 538 C; 627 G; 539 T; 0 U; 0 Other; 2327 313 121 121 225 126 Length:
Matches:
Conservative:
Mismatches: US-10-049-957-4 (1-738) x AAZ24196 (1-2327) 1.05e-103 1270.50 55.29% 39.87% 32.28% Best Local Similarity: Query Match: DB: Percent, Similarity: Alignment Scores 셤 ð

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379	ValAlaValArgArgSerSerHisValThrIleAspThrLeuLysGlyValLysSer 129
130 439	CyshisThrGylleAsnArgThrValGlyTrpAsnValProValGlyTyrLeuValGlu 149 :: ::: ::: TGCCACACGGGTCTAGGCAGGTCCGCTGGGTGGAACATCCCCATAGGTTTAC 495
150	SerGlyArgLeuSerValMetGlyCysAsp
163	AlavalSerAspTyrPheGlyGlySerCysValProGlyAlaGlyGluThrSerTyrSer 182 ::::::::
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223	AspvalalaphevallysHisSerThrValLeuGluAsnThrAspGlyLysThrLeuPro 242
243	SerTrpGlyGlnAlaLeuLeuSerGlnAspPheGluLeuLeuCysArgAspGlySer 261 :::
262	262 ArgAlaAspValThrGluTrpArgGlnCysHisLeuAlaArgValBroAlaHisAlaVal 281
282	ValvalargalaaspThraspGlyGlyleullePheArgLeuLeuAsnGlu 298
299 895	31
318	33
338	GlnThrTyrGluAlaTrpLeuGlyHisGluTyrLeuHisAlaMetLysGlyLeuLeu 356 ::: ::: ::
357	
366	LeudrgTrpCysValLeuSerThrProGluileGlnLysCysGlydspMetAlaValala 385
386	PheArgargGlnArgLeuLysProGluIleGlnCysValSerAlaLysSerProGlnHis 405AACAGTGTAGGGAAATAGAGTGTGTATCAGCAGAGACCCCGAAGAC 1215
406	CysMetGluargileGlnalaGluGlnValaspalaValThrLeuSerGlyGluaspile 42
426 1276	TyrthralaglybybybyglyteuvalproalaalaglygluhistyralaProglu 44

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                1333 GATAATTGTGAGGATACACCAGAGGCAGGCTATTTGCTGTAGCAGTGGTGAAGAAATCA
                               SerSerHisAlaPheThrLeuAspGluLeuArgGlyLygArgSerCygHisAlaGlyPhe
                                         ----agatttgatgattttttcagtgaaggttgtgcccct
                                                                                                                                    521 ValAsnAsnProLysAsnTyrProSerSerLeuCysAlaLeuCysValGlyAspGluGln
                                                                                                                                                                    GlyArgAsnLysCysValGlyAsnSerGlnGluArgTyrTyrGlyTyrArgGlyAlaPhe
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The invention relates to detecting (M1) granulocyte (GC) activation CC (GCA), by detecting the level of expression of gene (B) (GB) identified by DNA chip analysis as given in the specification, and comparing the DNA chip analysis as given in the specification, and comparing the expression level to an expression level in an unactivated GC, where additional expression of the least one gene in GB; (B) secreting (M2) GA by contacting GC with an agent that alters the expression of at least one gene in GB; (2) screening (M3) for an agent capable of modulating GGA or an inflammation (especially chronic) in a criser of graphs of a modulating GGA or an inflammation (especially chronic) in a pathogen or sterile inflammatory disease using the gene expression of the gene is indicative of genetially chronic) in a correcting (M4) an inflammation; (4) treating corresponse in a subject, exposure of a subject to a pathogen or sterile inflammatory disease, by detecting the level of expression of the gene is indicative of inflammation; (4) treating corresponse in a manulation; (4) treating corresponse in a subject, exposure of a subject or septime in a subject, exposure of a pathogen or sterile inflammatory disease, by detecting the level of expression of the gene is indicative of inflammation; (4) treating corresponse in a subject, exposure of a subject to a pathogen or sterile inflammation in a tissue, and tissue and the sequence of a pathogen or sterile inflammatory distress syndrome, inflammatory bowel disease, ulcerative colities, periodomical disease, ulcerative colities, periodomical disease, and the present sequence represents a gene di Detecting granulocyte activation by detecting differential expression of genes associated with granulocyte activation, which serves as diagnostic markers that is useful for monitoring disease states and drug toxicity. Human; ss; granulocytic cell; DNA chip; bacterial infection; viral infection; parasitic infection; protozoal infection; fungal infection; sterile inflammatory disease; psoriasis; rheumatoid arthritis; glomerulonephritis; asthma; thrombosis; cardiac reperfusion injury; renal reperfusion injury; ARDS; adult respiratory distress syndrome; inflammatory bowel disease; Crohn's disease; ulcerative colitis; periodontal disease; granulocyte activation; chronic inflammation; allergy. Sequence 2347 BP; 604 A; 555 C; 647 G; 540 T; 0 U; 1 Other; Vockley J; s, electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences Yamaga ID NO 743; 114pp; English. Weissman SM, 03-OCT-2000; 2000US-0237189P. 03-OCT-2001; 2001WO-US030821. (GENE-) GENE LOGIC INC WPI; 2002-435328/46. Beazer-Barclay Y, WO200228999-A2 Homo sapiens. Claim 1; SEQ 11-APR-2002

2347

Length: Matches:

1.06e-103 1270.50

604 A; 555 C; 647 G; 540 T; 0 U; 1 Other;

Sequence 2347 BP;

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progression of liver cancer, hepatocellular carcinoma or metastatic liver tumour in a patient, and differentiating metastatic liver cancer from hepatocellular carcinoma in a patient, involving detecting the level of expression of two or more genes represented in ABN3553-ABN3455 in a tissue sample. The method is useful for diagnosing and detecting cytostatic activity. The method is useful for diagnosing and detecting in the progression of liver cancer, hepatocellular carcinoma and metastatic liver carcinoma in a patient. The method is useful for identifying expression profiles which serve as useful diagnostic markers as well as markers that can be used to monitor disease states, disease progression, for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at the printed specification, but was obtained in the patent did not sequences.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The invention relates to a novel method for diagnosing and detecting the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gene; liver cancer; ds; hepatocellular carcinoma; hepatotropic; metastatic liver tumour; cytostatic; expression profile; disease state; disease progression; drug toxicity; drug efficacy; drug metabolism.
                                 1994 TGTTTGTTCCGGTCGGAAACC-----AAGGACCTTCTGTTCAGAGATGACACTA
                                                                                                             2045 IGTITGGCCAAACTICATGACAGAAACÁCÁTÁTGAAAAATACTTÁGGAGAAGAATÁTGTC
                                                                                                                                                   699 AlaAlaLeuGluGlyMetSerSerGlnGlnCysSerGlyAlaAlaAlaProAlaProGly
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LysMetPheAspSerSerAsnTyrHisGlyGlnAspLeuLeuPheLysAspAlaThrVal
                                                                         679 ArgAlaValProValGlyGluLysThrThrTyrArgGlyTrpLeuGlyLeuAspTyrVal
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                                                                                                                           80 ATGAGGCTCGCCGTGGGAGCCCTGCTGCTCTGCGCCTCTGGGGCTCTGGCTGTGT 139
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                                                                                                                                                           19 GlyGlyMetGluValArgTrpCysAlaThrSerAspProGluGlnHisLysCysGlyAsn
                                                                                                                                                                                                         39 MetSerGluAlaPheArgGlu-------AlaGlyIleGlnProSerLeu
                                                                                                                                                                                                                                                     53 LeuCysValArgGlyThrSerAlaAspHisCysValGlnLeuIleAlaAlaGlnGluAla
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                   Matches:
Conservative:
Mismatches:
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                                                      Indels:
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      1.06e-103
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learch completed: May 16, 2004, 20:04:59 ob time : 876 secs

Sequence 1

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ALIGNMENTS

RESULT 1
US-08-520-933-1
is Sequence 1, Application US/08520933
j Patent No. 5981194
j Patent No. 5981194
j APPLICANT: Wiffeed A. APPLICANT: WGGer, Patrick L. APPLICANT: Rood, Michael R. APPLICANT: Yamada, Tatsuo APPLICANT: Wennard, Malcolm TITLE OF INVENTION: Use of p97 and Iron Binding Proteins TITLE OF INVENTION: as Diagnostic and Therapeutic Agents NUMBER OF SEQUENCES: 11
j CORRESPONDENCE ADDRESS:
j STRPP"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SITKEL: 10 A ALING SLIEEL WEST.
CUNTRY: Canada
ZIP: MSH 3Y2
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/520,933
FILING DATE: August 31, 1995
CLASSIFICATION NUMBER: 31, 1995
CLASSIFICATION NUMBER: 38, 798
REGISTRATION NUMBER: 38, 798
REGISTRATION NUMBER: 38, 798
REGISTRATION NUMBER: 38, 798
TELECOMMUNICATION INFORMATION:
TELEPHONE: 416-364-7311
PCT US93 - 03614-1
US - 08 - 655 - 640-1
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Patent No. 5262177
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                                   GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
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Xgapop 10.0, Xgapext
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                                   LeuProSerTrpGlyGlnAlaLeuLeuSerGlnAspPheGluLeuLeuCysArgAspGly
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TELEFAX: 416-361-1398
TELEX: 06-23115
INPORMATION FOR SEQ ID NO: 1: SEQUENCE CHARACTERISTICS:
LENGTH: 2368 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPCLOGY: linear
MOLECULE TYPE: CDNA
HYPOTHETICAL: NO
FRATURE:
NAME/KEY: CDS
LOCATION: 61.117
FRATURE:
NAME/KEY: CDS
LOCATION: 118.2274
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COUNTRY: Canada
ZIREET: 40 King Street West
STREET: 40 King Street West
CITY: Toronto
STATE: Ontario
COUNTRY: Canada
ZIP: MSH 3Y2
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/285,040
FILING DATE: UJ-APR-1999
CLASSIFICATION: 435
ATTONEY/AGENT INPORMATION:
NAME: Gravelle Micheline
REGISTRATION NUMBER: 40,261
REFERENCE/DOCKET NUMBER: 7685-032
TELECOMMUNICATION INPORMATION:
TELEFORM: 416-364-7311
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Jefferies, wilfred A. APPLICANT: McGeer, Patrick L. APPLICANT: Rothenberger, Sylvia APPLICANT: Rothenberger, Sylvia APPLICANT: Food, Michael R. APPLICANT: Yamada, Tatsuo APPLICANT: Kennard, Malcolm TITLE OF INVENTION: Use of p97 and IrTITLE OF INVENTION: as Diagnostic and NUMBER OF SEQUENCES: 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 1, Application US/09285040 Patent No. 6455494 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEFAX: 416-361-1398
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH: 2368 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
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481 GlySerProAlaGlyTrpAspValProValGlyAlaLeuIleGlnArgGlyPheIleArg	Oy 501 ProlysAspOysAspValLeuThrAlaValSerGluPhePhaAshAlaSerCysValPro 520	521 ValAsnAsnProLysAsnTyrProSerSerLeuCysAlaLeuCysValGlyAspGluGln	Oy 541 GlyArgAsnLysCysValGlyAsnSerGlnGluArgTyrTyrGlyTyrArgGlyAlaPhe 560	Oy 561 ArgCysLeuValGluAsnAlaGlyAspValAlaPheValArgHisThrThrValPheAsp 580	Oy 581 AsnThrAsnGlyHisAsnSerGluProTrpAlaAlaGluLeuArgSerGluAspTyrGlu 600	Qy 601 LeuLeuCysProAsnGlyAlaArgAlaGluValSerGlnPheAlaAlaCysAsnLeuAla 620	Qy 621 GlnIleProProHisAlaValMetValArgProAspThrAsnIlePheThrValTyrGly 640	Qy 641 LeuLeuAspLysAlaGlnAspLeuPheGlyAspAspHisAsnLysAsnGlyPheLysMet 660	Qy 661 PheaspSerSeraenTyrHisGlyGlnaspLeuLeuPheLysAspalaThrValargala 680	Qy 681 ValProValGlyGluLysThrThyrArgGlyTrpLeuGlyLeuAspTyrValAlaAla 700	4 (¹)	Oy 721 LeuLeuProLeuLeuProAlaLeuAlaAlaArgLeuLeuProProAlaLeu 738	RESULT 4 US-08-175-158A-1 ; Sequence 1, Application US/08175158A ; Patent No. 5986067	; GENERATION: APPLICANT: FUNK, Walter D.; APPLICANT: MacGILLIVRAY, Ross T.A.; APPLICANT: MASON, Anne B.; APPLICANT: MASON, Anne B.	; APPLICANT: WOODWORTH, KOBETC C. ; TITLE OF INVENTION: RECOMBINANT TRANSFERRINS, TRANSFERRIN HALF- ; TITLE OF INVENTION: MOLECULES AND MUTANTS THEREOF ; NUMBER OF SEQUENCES 7 .; CORRESPONDED.	CORRESPONDED ADDRESSE: ADDRESSEE: LAHIVE & COCKFIELD STREET: 60 State Street, suite 510 CITY: Boston CITY: Massach	COMPUTER READABLE FORM:
361 CAAGAGGTCGGTACCTCTATTACGCCGTGGCTGTGGTCAGGAGGAGCTCCCATGTGACC 420 121 IleAspThrLeulysGlyValLysSerCysHisThrGlyIleAsnArgThrValGlyTrp 140	141 AsnValProValGlyTyrLeuValGluSerGlyArgLeuSerValMetGlyCysAspVal 160 	LeulyshlavalSerAspTyrPheGlyGlySerCysValProGlyAlaGlyGluThrSer 	181 TyrserGluSerLeuCysArgLeuCysArgGlyAspSerSerGlyGluGlyValCysAsp 200 	LysserProLeuGlukrgTyrTyrAspTyrSerGlyAlaPhekrgCysLeuAlaGluGly	221 AlaGlyAspValAlaPheValLySHisSerThrValLeuGluAsnThrAspGlyLysThr 240 	LeuProSerTrpGlyGlnAlaLeuLeuSerGlnAspPheGluLeuLeuCysArgAspGly 	SerargalaAspValThrGluTrpArgGlnCysHisLeuAlaArgValProAlaHisAla 	ValValValValAsgalahspThrAspGlyGlyLeuIlePheArgLeuLeuAsnGluGlyGln 	ArgLeuPheSerHisGluGlySerSerPheGlnMetPheSerSerGluAlaTyrGlyGln 	LysAspLeuLeuPheLysAspSerThrSerGluLeuValProlleAlaThrGlnThrTyr 	GlualafrpleuGlyHisGluTyrLeuHisAlaMetLysGlyLeuLeuCysAspProAsn 	ArgLeuProProTyrLeuArgTrpCysValLeuSerThrProGluileGlnLysC 	381 AspMetAlaValAlaPheArgArgGlnArgLeuLySProGluIleGlnCysValSerAla 400 	401 INSSETPROGINHISCYSMETGINARGILEGINALAGINGINVALASDALAVAITHREU 420 	421 SerGlyGluAspIleTyrThrAlaGlyLysTyrGlyLeuValProAlaAlaGlyGlu 440 	441 HistyrAlaproGluAspSerSerAsnSerTyrTyrValValAlaValValArgArgAsp 460 	461 SerSerHisAlaPheThrLeuAspGlubeuArgGlyLyBArgSerCysHisAlaGlyPhe 480

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1111 GTGAAGTGGTGTGGCCTGAGCCACCACGAGGCCTCAAGTGTGATGAGTGGAGTGTT--- 1167
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                  439 TGCCACACGGGTCTAGGCAGGTCCGCTGGGTGGAACATCCCCATAGGCTTACTTTAC--- 495
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                                                                                                                      AlaValSerAspTyrPheGlyGlySerCysValProGlyAlaGlyGluThrSerTyrSer 182
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| GCAGTGGCCAATTTCTTCTCGGGCAGCTGTGCCCCTTGTGCGGATGGGACGACTTCCCC
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313
121
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225
126
34
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Matches:
Conservative:
Mismatches:
Indels:
Gaps:
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/175,158A
FILING DATE: 28-DEC-1993
CLASSIFICATION: DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US 07/832,029
FILING DATE: 06-FEB-1992
ATTORNEY/AGENT INFORMATION:
NAME: DECONTA, Gillio A.
REGISTRATION NUMBER: UVI-005CP2
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 2327 base pairs
TYPE: nucleic acid
STRANDENBESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
FRATURE:
NAME/KEY: CDS
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55.29%
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Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; NAME/KEY:
; LOCATION:
US-08-175-158A-1
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Pred. No.:
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115 -----CAGAGTTTCCGCGACCATATGAAAAGCGTCATTCCATCCGATGGTCCCAGTGTT 168
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           COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
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Mismatches:
Indels:
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                                                                 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/848,760B
FILING DATE: 25-Jan-2001
CLASSIFICATION: <UNKNOWN>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length:
Matches:
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SEQUENCE DESCRIPTION: SEQ ID NO: 25:
US-08-848-760B-25
                                                                                                                                       PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/838,702
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MOLECULE TYPE: other nucleic acid
                                                                                                                                                                                                                              REGISTRATION NUMBER: 38,261
                                                                                                                                                                                                                                               REFERENCE/DOCKET NUMBER: TELECOMMUNICATION: (352) 375-8100
                                                                                                                                                                         FILING DATE: 09-APR-1997
ATTORNEY/AGENT INFORMATION:
NAME: PACE, DORAN R.
Floppy disk
                                                                                                                                                                                                                                                                                                   372-5800
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LENGTH: 2097 base pairs
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Best Local Similarity:
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Patent No. 6248721
GENERAL INFORMATION:
TITLE OF INVENTION: Animal Model For ENUMBER OF SEQUENCES: 33
CORRESPONDENCE ADDRESS:
ADDRESSE: Saliwanchik, Lloyd & Signeer: 2421 N.W. 41st Street, Su.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COUNTRY: United States of America
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	0y 581 AsiThrAsnGlyHisAsinSerGluProTrpAlaAlaGluLeuArgSerGluAspTyrGlu 600 1678 AAACAGGGGGAAAAAACCCTGGGCGAAATTGAATTGAAT	; CURRENT APPLICATION DATA: ; APPLICATION NUMBER: US/08/145,681 ; FILING DATE:
AlaValSerAspryrPheGlyGlySerCysValProGlyAlaGlyGluThrSerTyrSer		481 GLYSGFPFOALAGLYTPASPVALIFPFOVALGLYALACULIEGLNATGGLYPHELIEATG 500 1420 GGCAGAACCGCTGGCAACATCCCCATGGGCCTGCTCTACAATAAG 1467
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1035 -----CTTGGCTCCGGCTACTTCACTGCCATCCAGAACTTGAGGAAAAGTGAGGAGGAA 1088
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                                                                                      228 LysHisSerThrValLeuGluAsnThrAspGlyLysThrLeuProSerTrpGlyGlnAla 247
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1311 GCAGAGAACTACAAATCCCAACAAGGAGTGACCTGATCCTAACTGTGGGATAGACCT
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                                                                    TyrAspTyrSerGlyAlaPheArgCysLeuAlaGluGlyAlaGlyAspValAlaPheVal
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Matches:
Conservative:
Mismatches:
Indels:
Gaps:
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CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: MCGREGOC., MARTID.
REGISTRATION NUMBER: 29,329
REFERENCE/DOCKET NUMBER: 19928-0125
TELEPHONE: 713/229/1874
TELEPHONE: 713/229/1874
TELEPHONE: 713/229/1874
SEQUENCE CHARACTERISTICS:
LENGTH: 2360 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TYPE: MOLECULE TYPE: CDNA
"""DOPLOGY: linear
MOLECULE TYPE: CDNA
"""DOTHETICAL: NO
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510 ATTGAGGCA-----
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1263.00
52.23%
37.87%
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                                                                                                                                                                                                                                                                                                                           ORIGINAL SOURCE:
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140 TrpAsnValProValGlyTyrLeu--
DATA
                                                                                                                                                                                                                                                                                                              TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
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         APPLICATION NUMBER:
FILING DATE:
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Query Match:
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HYPOTHETICAL: N
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US-08-250-308-1
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                                                                                                           2031 AGACTCCATGGCAAAACAAAACATATGAAAAATATTTGGGACCACAGTATGTCGCAGGCATT 2090
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                                                                                        GlyAspyalAlaPheValArgHisThrThrValPheAspAsnThrAsnGlyHisAsnSer 587
                                                                                                                                                               GluProTrpAlaAlaGluLeuArgSerGluAspTyrGluLeuLeuCysProAsnGlyAla 607
                                                                                                                                                                                                                                                                                                                  MetValArgProAspThrAsnIlePheThrValTyrGlyLeuLeuAspLysAlaGlnAsp 647
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                                                                                                                                                                                                                                                                                                                                         AsnSerGlnGluArgTyrTyrGlyTyrArgGlyAlaPheArgCysLeuValGluAsnAla
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
APPLICANT: Conneely, Orla M.
APPLICANT: Conneely, Orla M.
APPLICANT: Headon, Denis R.
APPLICANT: O'Malley, Bert W.
TITLE OF INVENTION: Production of Recombinant Human
TITLE OF INVENTION: Lactoferrin
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fulbright & Jaworski Patent Department
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE: Fulbright & Jaworski Patent Department STREET: 1301 McKinney St.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SYSTEM: PC-DOS/MS-DOS
PatentIn Release #1.0, Version #1.25
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Patent No. 5571896
Patent No. 5571896
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  702 GluGlyMet-----
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ZIP: 77010-3095
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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STATE:
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93 GTTCAGTGGTGCACCGTATCCCAAACCCCGAGGCCCACAAAATGCTTCCAATGGCAAAGGAAT 152
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330 GAAAGACAGCCACGAACTCACTATTATGCCGTGGCTGTGATGAAGAAGGGCGGCAGCTTT 389
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Matches:
Conservative:
Mismatches:
Indels:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-10-049-957-4 (1-738) x US-08-250-308-1 (1-2360)
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US/08/250,308
                                          CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/873,304
                                                                                                    ATTORNEY AGENT 1992
ATTORNEY/AGENT INFORMATION:
NAME: Adler Ph. D., Benjamin A.
REGISTRATION NUMBER: 35,424
REFERENCE/DOCKET NUMBER: D5456
TELEFAM: 713651554
INFORMATION FOR SEQ ID NO: 1:
INFORMATION FOR SEQ ID NO: 1:
LENGTH: 2360 base pairs
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1263.00
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-----CTTGGCTCCGGCTACTTCACTGCCATCCAGAACTTGAGGAAAAGTGAGGAAA 1088
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| GCAGAGAACTACAAATCCCAACAAAGCAGTGACCCTGATCCTAACTGTGGATAGACCT 1370
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TGTAACCAGTGGAGT------GGCTTGAGCGAAGGCAGCGTGACCTGCTCC 1193
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          GAAAGACAGCCACGAACTCACTATTATGCCGTGGCTGTGGTGAAGAAGAGGGCGGCAGCTTT 389
                                                                               139
                                                                                                                                                                                                                                                                                                                                                             ValGluSerGlyArgLeuSerValMetGlyCysAspValLeuLysAlaValSerAspTyr 167
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TACGAGGCAGGCCTGGCCCCTACAAACTGCGACCTGTAGCGGCGGAAGTCTACGGGACC 329
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     43 PheArgGluAlaGlyIleGlnProSerLeuLeuCysValArgGlyThrSerAlaAspHis 62
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SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/453,703
FILING DATE: Concurrently herewith
CLASSITCATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/145,681
FILING DATE: October 28, 1993
ATTORNEY/AGENT INFORMATION:
NAME: Albert P. Halluin
REGISTRENCE/DOCKET NUMBER: 82.06-024
TELEPHONE: 415-84-366
TELEPHONE: 415-84-366
TELEPHONE: 415-84-369
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
TEMPTON AND SECTION:
SECUENCE CHARACTERISTICS:
TEMPTON AND SECTION OF SECTION OF
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Mismatches:
Indels:
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Matches:
TITLE OF INVENTION: Various Organisms NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS: ADDRESSEE: Pennie & Edmonds
                                                                                                                                                                                                                                                                          ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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52.23$
37.87$
32.09$
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TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                        1155 Avenue of
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY: linear
MOLECULE TYPE: cDNA
HYPOTHETICAL: NO
                                                                                                                                     STREET: 1155 Aver
CITY: New York
STATE: New York
COUNTRY: USA
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Best Local Similarity:
Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ANTI-SENSE: NO ORIGINAL SOURCE:
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Pred. No.:
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APPLICANT: Conneely, Orla M.
APPLICANT: Headon, Denis R.
APPLICANT: Headon, Denis R.
APPLICANT: O'Malley, Bert W.
APPLICANT: May, Gregory S.
TITLE OF INVENTION: Production of Recombinant Lactoferrin
TITLE OF INVENTION: and Lactoferrin Polypeptides Using cDNA Sequences in
TITLE OF INVENTION: Various Organisms
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-10-049-957-4 (1-738) x US-08-456-106-1 (1-2360)
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                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US/08/456,106
FILING DATE: Concurrently herewith
CLASSIPICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/145,681
FILING DATE: October 28, 1993
ATTORNEY/AGENT INFORMATION:
NAME: Albert P. Halluin
REGISTRATION NUMBER: 25,227
REFERENCE/DOCKET NUMBER: 8206-025
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-854,3660
                                                                                                                                                                       ADDRESSE: Pennie & Edmonds
STRET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    INFORMATION FOR SEQ ID NO: 1: SEQUENCE CHARACTERISTICS: LENGTH: 2360 base pairs TYPE: nucleic acid STRANDEDNESS: single
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Best Local Similarity:
GENERAL INFORMATION
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                                                                                                                                                                                                                                               COUNTRY:
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1932 AAATTTGGG------AGAAATGGATCTGACTGCCCGGACAAGTTTTGCTTATTC 1979
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            ----SerTyrTyrValValAlaValValArgArgAspSerSerHisAlaPheThrLeu
                                                                                AspGluLeuArgGlyLysArgSerCysHisAlaGlyPheGlySerProAlaGlyTrpAsp
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2360
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                                   Conservative:
Mismatches:
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Sequence 1, Application US/08456106 Patent No. 5849881

US-08-456-106-1

us-10-049-957-4.rni

83	TyrglualaglyLysgluHisglyLeuLysProValValGlyGluValTyr 99 TacgaGcCagGcCcCCTacaaaCrGcGaCCTGTAGCGGCGGAAGTCTACGGGACC 329	ò a à	419 ThrLeuSerGlyGluAspIleTyrThrAlaGlyLysLysTyrGlyLeuValProAlaAla 438 :::
100 AspGlnGluValG :::::::: 330 GAAAGACAGCCAC	AspGlnGluValGlyThrSerTyrTyrAlaValAlaValValArgArgSerSerHisVal 119 :::::::: GAAAGACAGCCACGAACTCACTATTATGCCGTGGCTGTGGTGAAGAAGGGCGGCAGCTTT 389	දු දි	GLYGIUMISHYZATARTOGLUASDSGESGIASH
120 ThrileAspThri -::::: 390 CAGCTGAACGAAC	ThrileAspThrLeuLy9GlyValLy8SerCy8HisThrGly11eAsnArgThrValGly 139 :::::	& g	SerTyrTyrValValAlaValValNzArgArgAspSerSerHisAlaPheThrLeu SerTyrTyrValValValValValValNzArgAspSerSerHisAlaPheThrLeu
140 TrpAsnValPro 450 TGGAATGTGCCT	TrpAsnvalProvalGlyTyrLeu	රු යි	AspGluLeuArgGlyLysArgSerCysHisAlaGlyPheGlySerProAlaGlyTrpAsp .:: :::
148 ValGluSerGlyArg ::: ::: 510 ATTGAGGCA	ValGluSerGlyArgLeuSerValMetGlyCysAspValLeuLysAlaValSerAspTyr 167 	ò a	488 ValProva/GlyAlaLeuileGlnArgGlyPheileArgFroLy8AspCy8AspValLeu 507 ::: :: 1188 1488 ATCCCCATGGGCCTGCTCTTCAACCAGACGGGCTCCTGC 1526
168 PheGlyGlyse	ValProGlyAlaGlyGluThrSerTyrSerGluSerLeuCysArg	ò q	508 ThralavalSerGluPhePheAsnalaSerCysValProValAsnAsnProLysAsnTyr 527
188 LeuCysArgG 591 Creneneed	LeuCysArgGlyAspSerSerGlyGluGlyValCysAspLysSerProLeuGluArgTyr 207 	ò a	528 ProSerSerLeuCysAlaLeuCysValGlyAspGluGlnGlyArgAsnLysCysValGly 547 :::
208 TyrAspTyrs :::		da Db	548 AsnSerGlnGluArgTyrTyrGlyTyrArgGlyAlaPheArgCysLeuValGluAsnAla 567
228 Lyshisser		λ _o q _o	568 GIVASpValAlaPheValArgHisThrThrValPheAspAsnThrAsnGlyHisAsnSer 587
248 LeuleuSerC 744GAAAGGC	rgalaaspvalThrGlu ::: GGAAGCCAGTGGACAAG	& 8	
268 TrpArgGlnC :::::	268 TrpArgGlnCysHisLeuAlaArgValProAlaHisAlaValValArgAlaAsp 286 ::::::	ò a	608 ArgAlaGluValSerGlnPheAlaAlaCysAsnLeuAlaGlnIleProProHisAlaVal 627
287 ThraspGlyC		ò da	628 MetValArgProAspThrAsnIlePheThrValTyrGlyLeuLeuAspLysAlaGlnAsp 647 :::
307 GlySerE		ò q	648 LeuPheGlyAspAspHisAsnLysAsnGly
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248 LeuLeuSerGlnAspPheGluLeuLeuCysArgAspGlySerArgAlaAspValThrGlu 267
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    43 PheArgGluAlaGly1leGlnProSerLeuLeuCysValArgGlyThrSerAlaAspHis 62
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                                                                                                                                                                                                                        excunction of Recombinant Lactoferrin and Lactoferrin Polypeptides Using cDNA Sequences in Various Organisms
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GTTCAGTGGTGCACCGTATCCCAACCCGAGGCCACAAAATGCTTCCAATGGCAAAGGAAT 152
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PatentIn Release #1.0, Version #1.25
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Conservative:
                                                                                                                                                      APPLICANT: Conneely, Orla M.
APPLICANT: Headon, Denis R.
APPLICANT: O'Walley, Bert W.
APPLICANT: May, Gregory S.
TITLE OF INVENTION: Production of Recombinant TITLE OF INVENTION: and Lactofertin Polypeptid ITLE OF INVENTION: Various Organisms
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mismatches:
Indels:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: Albert P. Halluin
REGISTRATION NUMBER: 25,227
REFERENCE/DOCKET NUMBER: 8206-023
TELEPRONE: 415-854-3660
TELEPRONE: 415-854-3694
INPORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
arcrectracaarrcccrecrer 2294
                                                                                                                                                                                                                                                                                                                                  ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/456,108
FILING DATE: Concurrently herewith
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
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FILING DATE: October 28, 1993
ATTORNEY/AGENT INFORMATION:
                                                                                           Sequence 1, Application US/08456108 Patent No. 6100054
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDIUM TYPE: Floppy disk COMPUTER: IBM PC COMPATIBLE OPERATING SYSTEM: PC-DOS/MS-SOFTWARE: Patentin Release #
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LENGTH: 2360 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
HYPOTHETICAL: NO
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ORIGINAL SOURCE:
ORGANISM: H. sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                             ZIP: 10036
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                           NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                        CITY: New York
STATE: New York
COUNTRY: USA
                                                                                                                                   GENERAL INFORMATION:
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Pred. No.:
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	5-577-1 No. 6228614 NO. 6228614 NINFORMATION: NANT: Conneely, ANT: Headon, I	INVENTION: PRO INVENTION: AND INVENTION: ORG INVENTE: 0138002: PPLICATION NUM ILING DATE: 19 SEQ ID NOS: 1.	Length:	1263.00 it Similarity: 52.23 Acal Similarity: 37.878 Match: 32.098 30.098	Oy 3 GlyProSerGlyAlaLeuTrpLeuLeuLeuAlaLeuArgThrValLeuGlyGlyMetGlu 22	Db 93 GTTCAGTGGTGCACCGTATCCCAACCGAGGCCACAAATGCTTCCAATGGCAAAGGAAT 152 Qy 43 PheArgGluAlaGlyIleGlnProSerLeuLeuCysValArgGlyThrSerAlaAspHis 62	63 CysValGlnLeuIleAlaAlaGlnGluAlaAspAlaIleThrLeuAspGlyGlyAlaIle	Oy 83 TyrGluAlaGlyLysGluHisGlyLeuLysFroValValGlyGluValTyr 99	Qy 120 ThrileAspThrLeuLysGlyValLysSerCysHisThrdlyIleAsnArgThrValGly 139 a::::: ::: :::
	439 GlyGluHisTyrAlaProGluAspSerSerAsn	468 AspGluLeuArgGlyLysArgSerCysHisAlaGlyPheGlySerProAlaGlyTrpAsp 487 1428 i::::: :::	1527AAATTTGATGATATTTCAGTCTAGCTCTTGGTCTTGACCCGAGA 1577 528 ProSerSerLeuCysAlaLeuCysValGlyAspGluGlnGlyArgAsnLySCysValGly 547 578TCTAATCTCTGTGTTTGGCGAGGGGGGGGGGGAGAATAAGTGCGTGC	548 AsnSerGinGluargTyrTyrGlyTyrArgGlyAlaPheArgCysLeuValGluAsnAla 567	588 GluProTrpAlaAlaGluLeuArgSerGluAepTyrGluLeuLeuCysProAsnGlyAla 607	1815 CGGAAGCCTGTGACTGAGGCTAGAAGCTGCCATTGCCATGGCCCCCGAATCATGCCGTG 1874 628 MetValArgProAspThrAsnIlePheThrValTyrGlyLeuLeuAspLysAlaGlnAsp 647 :::		662 AspSerSerAenTyrHisGlyGlnAepLeuleuPheLysAspAlaThrValArgAlaVal 681 1980 CAGTCTGAAACCAAAAACCTTCTGTTCAATGACACTGAGTGTCTGGCC 2030 682 ProValGlyGluLysThrThrTyrArgGlyTrpLeuGlyLeuAspTyrValAlaAlaLeu 701 2031 AGACTCCATGGCAAAACAACATATGAAAAATATTTGGGACCACAGTATGTCGCCGCAGGCCATT 2090	702 GluGlyMet 704 i i i i 2091 ACTAATCTGAAAAGCTCCCCCCCCCCCCCCCCCTGGAAGCCTGTGAATTCCTCAGGAAG 2150 704 704

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| GCAGAGAACTACAAATCCCAACAAGCAGTGACCCTGATCCTAACTGTGTGGGATAGACCT 1370
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| AAGGACTCTGCCATTGGTTTTCGAGGGTGCCCCCGAGGATAGATTCTGGGCTGTAC--- 1034
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GTGGAAGGATATCTTGCTGTGGCGGTGGTTAGGAGA---TCAGACACTAGCCTTACCTGG 1427
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                                                                                                   TICAAAAGACTGCCATCTGGCCCGGGTCCCTTCTCATGCCGTTGTGGCACGAAGTGTGAAAT
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                           LeuLeuSerGlnAspPheGluLeuLeuCysArgAspGlySerArgAlaAspValThrGlu
                                                                                    TrpArgGlnCysHisLeuAlaArgValProAlaHisAlaValValValArgAla---Asp
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                                                       ---caaagegacgagtargagtracrcreccagacaacacrcegaagccagregaga
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Mismatches:
Indels:
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Matches:
         CURRENT APPLICATION NUMBER: US/09/633,739
CURRENT FILING DATE: 2000-08-07
PRIOR PILING DATE: 1995-05-30
NUMBER OF SEQ ID NOS: 14
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 1
LENGTH: 2360
TYPE: DNA
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52.23%
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REFERENCE: 01380023US02
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US-09-633-739-1
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Best Local Similarity:
Query Match:
DB:
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 7136515587
TELEFAX: 7136515246
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1263.00
52.23%
37.87%
32.09%
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                         18..2153
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Best Local Similarity:
Query Match:
                                                                                                                                                                 TOPOLOGY..
MOLECULE TYPE: CF
                                                                                                                                                                                                  HYPOTHETICAL: 1
ANTI-SENSE: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Alignment Scores:
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1932 AAATTTGGG------AGAAATGGATCTGACTGCCCGGACAAGTTTTGCTTATTC 1979
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                                                  1755 GAGGCATGGGCTAAGGATTTGAAGCTGGCAGACTTTGCGCTGCTGCTGCCCTGATGGCAAA 1814
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1875 GTGTCTCGGATGGAT---AAGGTGGAACGCCTGAAACAGGTGCTGCTCCACCAACAGGCT 1931
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               GluProTrpAlaAlaGluLeuArgSerGluAspTyrGluLeuLeuCysProAsnGlyAla
                                                                                                                                                             628 MetValArgProAspThrAsnIlePheThrValTyrGlyLeuLeuAspLysAlaGlnAsp
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                                                                                       608 ArgAlaGluValSerGlnPheAlaAlaCysAsnLeuAlaGlnIleProProHisAlaVal
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STREET: 1301 McKinney St.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: PATENTIN Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                         648 LeuPheGlyAspAspHisAsnLysAsnGly-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2271 ATCTGCTTACAATTCCCTGCTGTC 2294
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 1, Application PC/TUS9303614
GENERAL INFORMATION:
APPLICANT: Conneely, Orla M.
APPLICANT: Headon, Denis R.
TITLE OF INVENTION: Production of Refine Production of TITLE OF INVENTION: Lactoferrin NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: PCT/US93/03614
FILING DATE: 19930416
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APPLICATION NUMBER: US/07/873,304
FILING DATE: 24-APR-1992
ATTORNEY/AGENT INFORMATION:
NAME: Adler Ph.D., Benjamin A.
REGISTRATION NUMBER: 35,423
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
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CITY: Houston
STATE: Texas
COUNTRY: USA
ZIP: 77010-3095
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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93 GTTCAGTGGTGCACCGTATCCCAACCCGAGGCCACAAAATGCTTCCAATGGCAAAGGAAT 152
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 23 ValArgTrpCysAlaThrSerAspProGluGlnHisLysCysGlyAsnMetSerGluAla 42
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306
116
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Matches:
Conservative:
Mismatches:
                                                                                                                                                                                                                                                                                                                                 FEATURE:
NAME/KEY: misc_RNA
LOCATION: 18..2153
LOCATION METHOD: experimental
OTHER INFORMATION: /product= "lactoferrin"
OTHER INFORMATION: /evidence= EXPERIMENTAL
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INFORMATION FOR SEQ ID NO: 1: SEQUENCE CHARACTERISTICS: LENGTH: 2360 base pairs TYPE: NUCLEIC ACID STRANDEDNESS: single TOPOLOGY: linear MOLECT
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| GCAGAGAACTACAAATCCCAACAAAGCAGTGACCCTGATCCTAACTGTGTGGATAGACCT 1347
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                                                                                                                                                          208 TyrAspTyrSerGlyAlaPheArgCysLeuAlaGluGlyAlaGlyAspValAlaPheVal 227
                                                                                                                                                                                                                                                                                                                                                                              TrpArgGlnCysHisLeuAlaArgValProAlaHisAlaValValValArgAla---Asp 286
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                                                                                                                                                                                                                                  LysHisSerThrValLeuGluAsnThrAspGlyLysThrLeuProSerTrpGlyGlnAla 247
                                                                                                                                                                                                                                                                                                          LeuLeuSerGlnAspPheGluLeuLeuCysArgAspGlySerArgAlaAspValThrGlu 267
                                                                                                                                                                                                                                                                                                                                                                                                    287 ThrAspGlyGlyLeuilePheArgLeuLeuAsnGluGlyGlnArgLeuPheSerHisGlu 306
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LysAspSerThr-----SerGluLeuValPro---IleAlaThrGlnThrTyrGlu 341
                                                                                                                                                                                 307 Glyser---SerPheGlmMetPheSerSerGluAlaTyrGlyGlnLysAspLeuLeuPhe
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682 AGAGAGACAGTGTTTGAGGACCTGTCAGACGAGGCT-------
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307 GAAAGACAGCACGAACTCACTATTATGCCGTGGCTGTGGTGAAGAAGGGGGGGCAGCTTT
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299
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28
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/655,640
FILING DATE: 30-MXY-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION NAMER: US/92,538
FILING DATE: December 17, 1992
ATORNEY/AGENT INFORMATION:
AMANE: SCOTT, WATSON T:
REGISTRATION NUMBER: 26,581
FERENCE/DOCKET NUMBER: WTS/5683/98019/SAP
TELEFAX: (202) 861-3000
TELEFAX: (202) 862-0944
TELEFAX: (202) 822-0944
TELEFAX: (21) 22-0944
INPORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 2117 Dase pairs
TYPE: nucleic acid
STRANDEDNESS: double
TYPE: nucleic acid
STRANDEDNESS: double
TYPE: NAME/KEY: CDS
LOCATION: 1.2117
US-08-655-640-1
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Conservative:
Mismatches:
Indels:
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Best Local Similarity:
Query Match:
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Length:
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REFERENCE/DOCKET NUMBER: WTS,
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 861-3000
TELEFAX: (202) 862-0944
TELEX: 6714627 CUSH
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 2124 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
FEATURE:
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1260.50
54.93%
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Best Local Similarity:
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                             528 ProSerSerLeuCysAlaLeuCysValGlyAspGluGlnGlyArgAsnLysCysValGly
                                                                                     AsnSerGlnGluArgTyrTyrGlyTyrArgGlyAlaPheArgCysLeuValGluAsnAla
                                                                                                        .612 AACAGCAACGAGAGATACTACGGCTACACTGGGGCTTTCCGGTGCCTGAGAATGCT
                                                                                                                                               GlyAspValAlaPheValArgHisThrThrValPheAspAsnThrAsnGlyHisAsnSer
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 ---AAATTTGATGAATATTTCAGTCAAAGCTGTGCCCCTGGGTCTGACCCGAGA----
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Patent No. 5948613

GENERAL INFORMATION:
APPLICANT: Pend, Christina
APPLICANT: Pendla, Timothy J.
TITLE OF INVENTION: HUMAN LACTOFERRIN
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
ADDRESSE:
ADDRESSE:
CUSHWAN, DARBY & CUSHWAN
STREET: 1100 NEW YORK AVE. N.W., NINTH FLOOR
CITY: WASHINGTON
CITY: WASHINGTON
COUNTRY: USA
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/655,640
FILING DATE: 30-MAY-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/992,538
FILING DATE: December 17, 1992
ATTORNEY/AGENT INFORMATION:
NAME: SCOTT, WATSON T.
REGISTRATION NUMBER: 26,581
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US-08-655-640-3
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| ATGAGAAAAAGTGCGT---GGCCCTCCTGTCAGCTGCATAAAGAGAGACTCCCCATCCAG 192
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TGTATCCAGGCCATTGCGGAAAACAGGGCCGATGCTGTGACCCTTGATGGTGGTTGTTCATA 252
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ValGluSerGlyArgLeuSerValMetGlyCysAspValLeuLysAlaValSerAspTyr 167
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                                                                                                                                                                                                                                                                                                                                                                    ValArgTrpCysAlaThrSerAspProGluGlnHisLysCysGlyAsnMetSerGluAla 42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 43 PheArgGluAlaGlyIleGlnProSerLeuLeuCysValArgGlyThrSerAlaAspHis
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                                                                                                                                                                                                                                                       GlyProSerGlyAlaLeuTrpLeuLeuLeuAlaLeuArgThrValLeuGlyGlyMetGlu
2124
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Qy 568 GlyA Db 1678 GGAG Qy 588 GluP Db 1738 GAGG Qy 608 ArgA Qy 628 MetV Qy 628 MetV Db 1915 AAAT Qy 662 AspS Db 1915 AAAT Qy 682 Prov Qy 702 GluG Db 2074 ACTA Qy 722 Leu Db 2107 CTG Db 2107 CTG Db 2107 CTG Search completed: Job time: 231 sec Job time: 231 sec	
128 Lymit sserThrival LeuGluksriff has polytysthricubrosertricity dinking search. The seasokock defortrice accordance acc	548 AsnSerGlnGluArgTyrTyrGlyTyrArgGlyAlaPheArgCysLeuValGluAsnAla 567
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earch completed: May 16, 2004, 23:37:13 ob time : 231 secs

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Copyright (c) 1993 - 2004 Compugen Ltd.
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May 16, 2004, 19:30:57; Search time 4867 Seconds (without alignments) 4528.105 Million cell updates/sec
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3936
1 MRGPSGALWILLALRTVLGG......APLLPLLLPALAARLLPPAL 738
OM protein - nucleic search, using frame_plus_p2n model
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Xgapop 10.0, Xgapext
Ygapop 10.0, Ygapext
Fgapop 6.0, Fgapext
Delop 6.0, Delext
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Perfect score:
Sequence:
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55026578 Total number of hits satisfying chosen parameters: Minimum DB seq length: 0 Maximum DB seq length: 200000000

27513289 seqs, 14931090276 residues

Searched:

-MODEL=frame-pan.model -DEV=x1h
-Q=/Ggn2_1/USPTO_spool/US10049957/runat_14052004_100250_1269/app_query.fasta_1.903
-D==BST__QFWT=faste_PSTFTX=rst_MINMATCH=0.1.-LGODECL=0_LCODEXT=0
-DESST_QFWT=faste_PSTFTX=rst_MINMATCH=0.1.-LGODECL=0_LCODEXT=0
-UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-DOCALIGN=200 -TRR SCORE=pct -THR MAX=100 -TRR MIN=0 -ALIGN=15. MODE=LOCAL
-OUTFWT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=200000000
-USER=US10049957_GCGN 1 1 1906_@runat_14052004 100250_1269 -NCPU=6 -ICPU=3
-NO_MWAP -LARGEQUERY -NGG_SCORES=0 -WAIT -DSPELOCK=100 -LONGLOG
-EDST_TIMEOUT=120 -WARN TIMEOUT=30 -THRADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries Command line parameters:

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ALIGNMENTS

	mRNA linear HTC 19-SEP-2003	h enriched	noma associated)	identified by monoclonal antibodies 133.2 and 96.5, full insert							Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
;	linear	Mus musculus adult male bone cDNA, RIKEN full-length enriched	en p97 (mela	.2 and 96.5,							Vertebrata;
	yp mrna	DNA, RIKE	luct:antige	odies 133							Craniata;
	4055 bp	nale bone c	108P05 prod	lonal antib			1403		mouse)		Chordata;
		lus adult n	:lone:98301	by monoc]			AK036444.1 GI:26331403	rapper.	Mus musculus (house mouse)	lus	; Metazoa;
	AK036444	Mus muscu]	library, o	identified	sequence.	AK036444	AK036444.1	HTC; CAP trapper.	Mus muscu]	Mus musculus	Eukaryota
AK036444	rocus	DEFINITION				ACCESSION	VERSION	KEYWORDS	SOURCE	ORGANISM	

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LKAVGDY FGGSCVPGTGETSHSESLCRLCRGDSSGHNVCDKS PLERYYDYSGAFRCLA EGAGDVAFVKHSTVLENTDGNTL.PSWGKSLMSEDFQLLCRDGSRADITEWRRCHLAKV PAHAVVYGDNDGGL FQLLNEGQLLFSHEDSSFQMFSKRAYSGKNLLFKDSTLELVP TATQNYFAMLGGYLQAMKGLLCDPRLF.PHYLRWCVLSAPEIQKCGDMAVAFSRQNLK PEIQVSABESPEHCNEQIQAGHTDAYTLRGEDIYRACKYYGLVPAAGELYAEDRSNS YFVVAAVARRDSSYSFTLDELRGKRSCHPYLGSPAGWEVPIGSLIQRGFIRPKDCDVLT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AGDVAFVKHTTVFENTNGHNPEPWASHLRWQDYELLCPNGARAEVDQFQACNLAQMPS
HAVMVRPDTNI FTVYGLLDKAQDLFGDDHNKNGFQMFDSSKYHSQDLLFKDATVRAVP
VREKTTYLDWLGPDYVVALEGMLSQQCSGAGAAVQRVPLLALLLLTLAAGLLPRVL"
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GAGIRPSLLCVQGNSADHCVQLIKEQKADAITLDGGAIYEAGKEHGLKPVVGEVYDQD
IGTSYYAVAVVRRNSNVTINTLKGVKSCHTGINRTVGWNVPVGYLVESGHLSVMGCDV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AVSOFFNASCVPVNNPKNYPSALCALCVGDEKGRNKCVGSSOERYYGYSGAFRCLVEH
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                                                                                                                                                 /tissue_type="bone"
/clone_lib="RIKEN full-length enriched mouse cDNA library
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AlaileTyrGluAlaGlyLysGluHisGlyLeuLysProValValGlyGluValTyrAsp 100
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/note="unnamed protein product; antigen p97 (melanoma fnoce="unnamed protein py monoclonal antibodies 133.2 associated) identified by monoclonal antibodies 133.2 96.5 (MGD|MGI:1353421, GB|NM_013900, evidence: BLASTN, 99%, match=4055)
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Conservative:
Mismatches:
Indels:
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|db_xref="taxon:10090"
|clone="9830108P05"
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Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNa.

In Nature 420, 563-573 (2002)

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Direct Submission

L Submitted (16-UIJ-2001) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama, Institute, I.-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:genome-resegescriken:go;)

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                                                                                                                                                                                                                                 Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y. Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes 60000me Res. 10 (10), 1617-1630 (2000)
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   dammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     the RIKEN Genome Exploration Research Group Phase II Team and the
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FANTOM Consortium.
Functional annotation of a full-length mouse cDNA collection
Nature 409, 685-690 (2001)
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URL:http://fantome.gsc.riken.go.jp/
URL:http://fantom.gsc.riken.go.jp/.
Location/Qualifiers
                                                       Carninci, P. and Hayashizaki, Y.
High-efficiency full-length cDNA cloning
Meth. Enzymol. 303, 19-44 (1999)
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	Oy 389 GlnArgleuLysProGlu Oy 389 GlnArgleuLysProGlu Db 961 CAGGGGTCAAGCCAGAG Oy 409 ArglleGlnAlaGluGli Db 1021 CAGGAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG	429 GIVLYSLVSTY 1081 GGGAAACGEE	1141 1141 469	Db 1201 GAGCTTCGGGGCAAGCG Qy 489 ProValGlyAlaLeulle	Oy 509 AlaValSerGluPhePhe	1381 549 1441	Oy 569 AspValAlaPheValArd	1561 609 1621 629 1681	RESULT 3 AY420524 LOCUS DEFINITION Mus musculus MFI2 ge genomic survey seque ACCESSION AY420524 VERSION AY420524 KEYWORDS GSS.
COMMENT This sequence as made by sequencing genomic exons and ordering them based on alignment. FEATURES Location/Qualifiers 1.1734 1.1734 Aorganism="Homo sapiens" /mol_type="genomic DNA" /db_xref="taxon:9606" /gene="MFI2" /locus_tag="HCM7252" ORIGIN	Alignment Scores: Pred. No.: Score: Score: Pest Local Similarity: Query Match: 23.55.00 Matches: 463 Assacrative: Conservative: Minatches: 115 Query Match: 29.34* Indels: OB:	US-10-049-957-4 (1-738) x AY420522 (1-1734) Qy 69 AlaGlnGluAlaAspAlatleThrLeuAspGlyGlyAlatleTyrGluAlaGlyLysGlu 88	Qy 89 HisGlyLeuLysProvalValGlyGluValTyrAspGlnGluValGlyThrSerTyrTyr 108	Db 121 NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN	149 GluSerGlyArgLeuSerValMetGlyCysAspValLeuLysAlaValSerAspTyrPhe 241 NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN	169 GlyGlySerCysValProGlyAlaGlyGluThrSerTyrSerGluSerLeuCysArgLeu 301 NINNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN	Db 361 NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN	481 CACAGCACGCTACTICACTORING TO THE CACAGCACGCCAGGCCCTCCTCCTCCTCCTCCTCCTCCTCCTCCTCCTCCTC	Db 601 AGGCAGTGCCCGGGTGCCTGCTCACGCCGTGGTCGGGCCGACACAGAT 660 Qy 289 GlyGlyLeuIlePheArgLeuLeuAsnGluGlyGlnArgLeuPheSerHisGluGlySer 308

1734 bp DNA linear GSS 17-DEC-2003 gene, VIRTUAL TRANSCRIPT, partial sequence, uence. 1380 1500 heAlaAlaCysAsnLeuAlaGlnIleProProHisAlaValMet 628 528 568 348 368 840 900 rolleAlaThrGlnThrTyrGluAlaTrpLeuGlyHisGluTyr CCATCGCCACACAGACCTATGAGGCGTGGCTGGGCCATGAGTAC heasnalaSerCysValProValAsnasnProLysAsnTyrPro SnllePheThrValTyrGlyLeuLeuAspLysAlaGln 646 76481 us-10-049-957-4.rst

121 NINNINNINNINNINNINNINNINNINNINNINNINNIN	129 SerCysHisThrGlyIleAsnArgThrValGlyTrpAsnValProValGlyTyrLeuVal 148	181 NININININININININININININININININININI	149 GluSerGlyArgLeuSerValMetGlyCysAspValLeuLysAlaValSerAspTyrPhe 168	241 NININININININININININININININININININI	169 GlyGlySerCysValProGlyAlaGlyGluThrSerTyrSerGluSerLeuCysArgLeu 188	301 NININININININININININININININININININI	189 CysArgGlyAspSerSerGlyGluGlyValCysAspLysSerProLeuGluArgTyrTyr 208	361 NINDHANNANANANANANANANANANANANANANANANANAN	209 AspTyrSerGlyAlaPheArgCysLeuAlaGluGlyAlaGlyAspValAlaPheValLys 228	421 NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN	229 HisserThrValLeuGluAsnThrAspGlyLysThrLeuProSerTrpGlyGlnAlaLeu 248	LeuSerGlnAspPheGluLeuCySArgAspGl3148erArgAlaAspClTrp	541 CTGTCACAGGACTTTGAGCTGCTGTGCCGGGATGGTAGACGGGCCGACGTCACCGAGTGG 600	ArgGlnCysHisLeualaArgValProAlaHisAlaValValValArgAlaAspThrAsp	601 AGGCAGTGCCATCTGGCCCGGGTGCCTGCTCACGCCGTGGTGGTCCGGGCCGACACAGAT 660	289 GlyGlyLeuIlePheArgLeuLeuAsnGluGlyGlnArgLeuPheSerHisGluGlySer 308 	309 SerPheGlnMetPheSerSerGluAlaTyrGlyGlnLysAspLeuLeuPheLysAspSer 328	721 NIMINIMINIMINIMINIMINIMINIMINIMINIMINIM	329 ThrSerGluLeuValProlleAlaThrGlnThrTyrGluAlaTrpLeuGlyHisGluTyr 348	781 NIMININININININININININININININININININ	349 LeuHisAlaMetLysGlyLeuLeuCysAspProAsnArgLeuProProTyrLeuArgTrp 368	841 NINDHINDHINDHINDHINDHINDHINDHINDHINDHIND	369 CysValLeuSerThrProGluIleGlnLysCysGlyAspMetAlaValAlaPheArgArg 388	901 NININININININININININININININININININI	.389 GlnArgLeuLysProGluIleGlnCysValSerAlaLysSerProGlnHisCysMetGlu 408	961 NINNHANNINHANNINHANNINHANNINHANNINHANNINHANNINHANNINHANNINHANNINHAN 1020	409 ArgileGlnAlaGluGlnValAspAlaValThrLeuSerGlyGluAspIleTyrThrAla 428	1021 NNNNNNNNGCTGAGCAGGTCGACGCTGTGACCCTGAGTGGCGAGGACATTTACACGGCG 1080	429 GlyLysLysTyrGlyLeuValProAlaAlaGlyGluHisTyrAlaProGluAspSerSer 448	449 AsnSerTyrTyrValValAlaValValArgArgAspSerSerHisAlaPheThrLeuAsp 468	1141 AACTCGTACTGGTGGCGGTGGTGGTGGGGACAGCTCCCACGCCTTCACCTTGGAT 1200	469. GluLeuArgGlyLysArgSerCysHisAlaGlyPheGlySerProAlaGlyTrpAspval 488
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following 5' adaptor: GGCACGAG(G). Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH_MGC Library."	Alignment Scores: 1.02e-119 Length: 1023 Pred. No.: 1245.00 Matches: 235 Score: 1245.00 Matches: 235 Percent Similarity: 98.76% Conservative: 3 Best Local Similarity: 97.51% Mismatches: 3 Query Match: 13.63% Gaps: 0	US-10-049-957-4 (1-738) x BU185213 (1-1023) Qy	Qy 21 MetGluValArgTrpCysAlaThrSerAspProGluGlnHisLysCysGlyAsnMetSer 40	41 GlualaPheArgGlualaGlyIleGlnProSerLeuLeuCysValArgGlyThrSerAla	or Application of the control of the	81 AlailefyrGlublaGjyLysGluHisGlyLeuLysProValValGjyGluValTyrAsp 10 	Qy 101 GlnGluValGlyThrSerTyrTyrAlaValAlaValArgArgSerSerHisValThr 120 	Qy 121 IleAspThrLeuLysGlyValLysSerCysHisThrGlylleAsnArgThrValGlyTrp 140	Oy 141 AsnvalBrovalGlyTyrLeuValGluSerGlyArgLeuSerValMetGlyCysAspVal 160	Qy 161 LeulysAlaValSerAspTyrPheGlyGlyGlyThrSer 180	Qy 181 TyrSerGluSerLeuCysArgLeuCysArgGlyAspSerSerGlyGluGlyValCysAsp 200	Oy 201 LysSerProLeuGluArgTyrTyrAspTyrSerGlyAlaPheArgCysLeuAlaGluGly 220	Oy 221 AlaGlyAspValAlaPheValLy8HisSerThrValLeuGluAsnThrAspGlyLy8Thr 240	750 241 241 810	RESULT 6 BQ929045 LOCUS BQ929045 DEFINITION AGENCOURT_8967315 NCI_CGAP_Mam2 Mus musculus cDNA clone
ATGTC euThr rcaca	1321 GINININININININININININININININININININ	549 Serving Margivary Given Translate Analysis Serving Margivarian	DD 1501 GACGTIGCCTICGICAGGGCACACACGICTTIGACAACACAAANNNNNCAATTCCGAG 1560 QY 589 ProTrpAlaAlaGluLeuArgSerGluAspTyrGluLeuLeuCysProAsnGlyAlaArg 608 DD 1561 CCCTGGGCTGAGCTCAGGTCAAGGACTATGAACTGCTGTGCCCCAACGGGGCCCNN 1620		Qy 629 ValargProAspThrAsnIlePheThrValTyrGlyLeuLeuAspLysAlaGln 646 Db 1681 NTCCGGCCCGACACACATCTTCACCGTGTATGGACTGCTGGACAAGGCCCAG 1734		<u>о</u>	S EST. Homo sapiens (human) ISM Homo sapiens	BUNALTOLE; MCCAZOA; PINOIGACA; CIANIANA; VETCEDIANA; MAMMANIA; BUTHERIA; PLIMATES; CATATRINI; HOMINIAAE; HOMO. REFERENCE 1 (bases 1 to 1023) AUTHORS NIH-MGC http://mgc.ni.nih.gov/. TITTE NATIONAl Institutes of Health Mammalian Gene Collection (MGC)	Unpublished (1999) Contact: Robert Strausberg, Ph.D. Email: cgapbs r@mail.nih.gov	Laboratory 1.A.G.E. Consortium (LLNL) Secience Corporation	CIONE WISTIDATION: MAC CIONE WISTIDALION INFORMATION CAN DE found through the T.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Plate: LLCW1313 row: n column: 10 High musity sequence error. 603	FEATURES Location/Qualifiers source 1. 11023 /Ordanism="Homo sanions"	/organism= nowo saplens /mol_type="maker" /db_xref="taxon:9606" /clone="IMAGE:5952201" /tissue_type="ductal carcinoma, cell line"	/lab_host="DH10B" (phage-resistant)" /clone_lib="NIH_MGC_110" /note="Organ: pancreas; Vector: poTB7; Site_1: XhoI; Site_2: EcoR1; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the

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567 200 627 220 747 260

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AGENCOURT_8076230 NIH_MGC_110 Homo sapiens cDNA clone IMAGE:6084899 BU168950
                                                                                                                                                           LeuLysAlaValSerAspTyrPheGlyGlySerCysValProGlyAlaGlyGluThrSer 180
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(Dases 1 to 998)

NIH-MGC http://mgc.nci.nih.gov/.

National institutes of Health, Mammalian Gene Collection (MGC)

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATC
cDNA Library Preparation: Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
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High quality sequence stop: 626.
TyrSerGluSerLeuCysArgLeuCysArgGlyAspSerSerGlyGluGlyValCysAsp
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Library constructed by Life Technologies. Investigator
providing samples: Gilbert Smith, NIH"
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                                                                                            Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus. (Dases 1 to 937)

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National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)

Contact: Robert Strausberg, Ph.D.
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                                                                                                                                                                                                                                   Email: cgapbs-remail.nih.gov
Tissue Procurement: Gilbert Smith, Ph.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.B. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can b
found through the I.M.A.G.B. Consortium/LLNL at:
Pittp://image.llnl.gov
Http://image.llnl.gov
High quality sequence stop: 670.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

E 1 (Dases 1 to 819)

S NIH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

L'Onpublished (1999)

Contact: Robert Strausberg, Ph.D.

Emall: cgapbs-r@mail.nih.gov

Tissue Procurement: ATCC/DCTD/DTP

CDNA Library Preparation: Ling Hong/Rubin Laboratory

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LINL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LINL at: image.llnl.gov

Plate: LiCM137 row: m column: 12

High quality sequence stop: 722.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /organiam="Homo sapiens"
/mol_type="mRNA"
/mol_type="mRNA"
/mol_type="mRNA"
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/clone="INAGE:3347123"
/tissue_type="melanotic melanoma"
/lab.hofe="minto grape resistant)"
/clone lib="NIH MGC 20"
/note="Organ: Kin; Vector: pOTB7; Site_1: Xho1; Site_2: ECCR1; cDNA made by oliqo-dT priming. Directionally cloned into EccR1/Xho1 sites using the following 5; adaptor: GGCACGG(G). Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of Galifornia, Berkeley) using ZABP-CNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies)."
                    BE274850 819 bp mRNA linear EST 13-JUL-2000 601122847F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3347123 5',
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/note="Organ: pancreas; Vector: pOTB7; Site_1: XhoI; Site_2: ECORI; cDNA made by oligo-dT priming.
Directionally cloned into ECORI/XhoI sites using the following 5' adaptor: GGCACGAG(G). Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-CDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies).
Note: this is a NIH_MGC Library."
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cDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: National Institutes of Health Intramural
Sequencing Center (NISC),
Gaithersburg, Maryland;
Web site: http://www.nisc.nih.gov/
Contact: nisc_mgc@nhgri.nih.gov/
Contact: nisc_mgc@nhgri.nih.gov/
Contact: National Contact: National
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LiNL at: http://image.llnl.gov Series: IRAK Plate: 127 Row: c Column: 13
This clone has the following problem: no 5' EST match.
Location/Qualifiers
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                                                                               Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Lothar Hennighausen Ph.D., Priscilla Furth
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302
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NIH-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
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/lab_host="DH10B"
/note="Vector: pCMV-SPORT6"
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/mol_type="mRNA"
/strain="NMRI"
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/clone="IMAGE:5388731"
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

I (bases 1 to 2313)

Strausberg, R. L., Feingold, E. A., Grouse, L. H., Derge, J. G.,

Alschul, S. F., Zeeberg, B., Buetow, K. H., Schemmen, C. M., Schuler, G. D.,

Alschul, S. F., Jordan, H., Moore, T., Max, S. I., Wang, J., Hsieh, F.,

Diatchenko, L., Marusina, K., Farmer, A. A., Rubin, G. M., Hong, L.,

Stapleton, M., Soares, M., B., Bonaldo, M.F., Casavant, T. L.,

Scheetz, T. E., Brownstein, M. J. Usdin, T. B., Toshiyuki, S.,

Carninci, P., Prange, C., Raha, S. S., Loquellano, N. A., Peters, G. J.,

Abramson, R. D., Mullahy, S. J., Bosak, S. A., McEwan, P. J.,

Morley, K. C., Hale, S., Garcia, A. M., Gay, L. J., Hulyk, S. W.,

Villalon, D. K., Muzny, D. M., Sodergren, E. J., Lu, X., Gibbs, R. A.,

Bouffard, G. G., Blakesley, R. W., Touchman, J. W., Green, E. D.,

Butterfield, Y. S., Krzywinski, M. I., Schlska, U., Saniutz, J., Myers, R. M.,

Butterfield, Y. S., Krzywinski, M. I., Schlska, U., Saniuts, D. E.,

Schnerch, A., Schein, J. E., Jones, S. J. and Marra, M. A.

Mennand and marra, A. M. A. M. A. M. A. M. A. M. M. Sodergren, E. J., Myers, R. M.,

Butterfield, Y. S., Krzywinski, M. I., Schlska, U., Sanius, D. E.,

Generation and initial analysis of more than 15,000 full-length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 17-DEC-2003
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Submitted (15-SEP-2003) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
GlnGluValGlyThrSerTyrTyrAlaValAlaValValArgArgSerSerHisValThr
                                                                                                                                                                  121 IleAspThrLeuLysGlyValLysSerCysHisThrGlylleAsnArgThrValGlyTrp
                                                                                                                                                                                                                            TyrSerGluSerLeuCysArgLeuCysArgGlyAspSerSerGlyGluGlyValCysAsp
                                                    350 CAAGAGGTCGGTACCTCCTATTACGCCGTGGCTGGGGTCAGGAGGAGGACCCCATGTGACC
                                                                                                                                                                                                                                                                                                                                                                                               410 AACGIGCCCGIGGGCTACCIGGIGGAGAGAGCGCCCCCTCTCGGIGAITGGGCIGCGAIGIA
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Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
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TITLE
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Qy 453 ValValAlaValValArgArgAspSerSerHisAlaPheThrLeuAspG	-	Oy 473 LyahrgSerCysHisAlaGlyPheGlySerFroAlaGlyTrpAspValP:	Qy 493 LeulleGlnArgGlyPheileArgProLysAspCysAspValLeuThrA.	Qy 513 PhePheAsnAlaSerCysValProValAsnAsnProLysAsnTyrProSon	Qy 533 AlaLeuCysValGlyAspGluGlnGlyArgAsnLySCysValGlyAsnSe	Oy 553 TYrTyrGlyTyrArgGlyAlaPheArgCysLeuValGluAsnAlaGlyAe 	Oy 573 ValargHisThrThrValPheAspAsnThrAsnGlyHisAsnSerGluPh	Qy 593 GluLeuArgSerGluAspTyrGluLeuLeuCysProAsnGlyAlaArgAl	Oy 613 GlnPheAlaAlaCysAsnLeuAlaGlnIleProProHisAlaValMetVent	Qy 633 ThrAsnIlePheThrValTyrGlyLeuLeuAspLysAlaGlnAspLeuPh 	Qy 653 HisAsniysAsnGlyPheLysMetPheAspSerSerAsnTyrHisGlyG] bb 1930 GACTGCACGGCAATTCTGTTTGAAGTCTACGACCACCA	Oy 673 PheLyshspalaThrValArgAlaValProValGlyGluLysThrThThThThTh::	Qy 693 LeuGlybeuAspTyrValAlaAlaLeuGluGlyMetSerSerGlnGlnCh	Oy 713 AlaAla	722		RESULT 10 BC020295 LOCUS LOCUS BC020295 LOCUS DEFINITION Mus musculus transferrin, mRNA (cDNA clone IMAGE:396	ACCESSION BC020295. VERSION BC020295.1 GI:17946865 KEYWORDS HTC. SOURCE Mus musculus (house mouse)	
	112 ValValArgArgSerSerHisValThrIleAspThrLeuLysGlyValLysSerCysHis 131 391 GTGGTAAAGAAGGAAAGAGATTCCAGCTGAACAGGCAAGAAGTCCTGCAC 450	7alGlyTyrLeuValGluSerGly	ArgleuservalMetGlyCysAspValleuLysAlaValSerAspTyrPheGlyGlySer 	505 AAGCTGTCGGAGCCCCCCAGTCCTTGAGAAAGCTGTGTCCAGTTTCTTCTCGGGCAGT 564 172 CysValProGlyAlaGlyGluThrSerTyrSerGluSerLeuCysArgLeuCysArgGly 191	AspSerSerGlyGluGlyValCysAspLysSerProLeuGluArgTyrTyrAspTyrSer	GlyAlaPheArgCysLeuAlaGluGlyAlaGlyAspValAlaPheValLysHisSerThr	ValLeuGluAsnThrAspGlyLysThrLeuProSerTrpGlyGlnAlaLeuLeuSerGln ::::	AspPheGluLeuLeuCysArgAspGlySerArgAlaAspValThrGluTrpArgGlnCys	HisLeuAlaArgValProAlaHisAlaValValArgAlaAspThrAspGlyGly ::: -			SerGluLeuValProIleAlaThrGlnThrTyrGluAlaTrpLeuGlyHisGluTyr ::: :::	LeuHisAlaMetLysGlyLeuLeuCysAspProAsnArgLeuProPro	1051 GTCACTGCCATTCGGAATCAGCAAGGAAGGCGTGTGCCCGGAGGGCTCGATCGA	ccagraaardargracactgaarcaccragaagaaccaagrargacgagagagacarr	385 AlarheArgArgGinArgLeULYSProGillieGinCysValSerFalySerProGin 404 1171 ATCAGTGAGGGAAAGATAGAGTGTGAGTGCAGAGACACCACTGAG 1215	405 HiscysmetGluargIleGlnalaGluGlnValAspalaValThrLeuSerGlyGluasp 424	425 IleTyrThrAlaGlyLysLysTyrGlyLeuValProAlaAlaGlyGluHisTyrAlaPro 444	445 GludspSerSerAsn
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nCysSerGlyAla 712 |-||||||| |GTGCTCAACCTCA 2094 oGlubeuArgGly 472 : |||:::||| CAACCTGAAAGGC 1440 SerSerLeuCys 532 ||||:::|||||| -TCCACCCTCTGT 1587 SerGlnGluArg 552 :::::||| :ACAAAGAGGAA 1635 ProvalGlyAla 492 ValArgProAsp 632 ||||||| | TTTGGGGGAAGT 1929 GlnAspLeuLeu 672 :::||||||||| .AAGGACCTTCTG 1980 AAATTCGATGAA 1536 ||||||| GAATGGGCTAAG 1752 AAGCCTGTGAAA 1812 CCTGAAAATAC 2040 GlyAlaProLeu 721 HTC 17-DEC-2003 (968762). AlaValSerGlu 512 ProfrpAlaAla 592 AlaGluValSer 612 PheGlyAspAsp 652 TyrArgGlyTrp 692 a; Euteleostomi; ae; Murinae; Mus. 66

111 393

213

54

273

93

74

453

AUTHORS TITLE JOURNAL PUBMED REFERENCE JOURNAL

TITLE

REMARK

COMMENT

507

191 624 231

251

567

271

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Pred. No.:

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ORIGIN

FEATURES

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ValvalArgArgSerSerHisValThrIleAspThrLeuLysGlyValLysSerCysHis 131
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                                                                                               CCTGACAAAACGGTCAAATGGTGCGCAGTGTCAGAGCACGAGAATACCAAATGCATCAGC 159
                                                                                                                                                                         160 TTCCGTGACGACATGAAGACCGTCCTTCCGCCTGATGGC-----CCCCGGGCTTGCCTGT
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Klausner, R.D., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D., Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K., Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Hsieh, F., Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L., Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L., Scheetz, T.B., Brownstein, M.J., Usdin, T.B., Toshiyuki, S., Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J., Morenan, K.J., Malek, J.A., Gunarane, P.H., Richards, S., Worley, K.C., Hale, S., Garcia, A.M., Sodergren, E.J., Lu, X., Gibbs, R.A., Fahey, J., Halton, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A., Fahey, J., Halton, E., Ketteman, M., Madan, A., Rodrigues, S., Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shevchenko, Y., Butterfield, Y.S., Kazywinski, M.I., Skalska, U., Sanilus, D.E., Schnerch, A., Schein, J.E., Jones, S.J., and Marra, M.A., Schein, J.E., Jones, S.J., and Marra, M.A., Schein, J.E., Jones, S.J., and Marra, M.A., and mouse of Nakasana and mouse of Nakasana and manyeis of more than 15,000 full-length
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Direct Submission
Submitted (20-DEC-2001) National Institutes of Health, Mammalian
Gene Collection (MCC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Clone distribution: MGC clone distribution information can be fou through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Series: IRAK Plate: 40 Row: h Column: 16 This clone has the following problem: no 5' EST match. Location/Qualifiers
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/clone="IMAGE:3968762"
/tlsue type="Mammary tumor. Metallothionien-TGF alpha model. Io month old virgin mouse. Taken by biopsy."
/clone lib=NCI CGAP_Mam1"
/lab_bost="DH10B"
/note="Vector: pCMV-SPORT6"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Center code: BCM-HGSC
Web site: http://www.hgsc.bcm.tmc.edu/cdna/
Contact: amg@bcm.tmc.edu
Gunaratne, P.H., Garcia, A.M., Lu, X., Hulyk, S.W., Loulseged, Kowis, C.R., Sneed, A.J., Martin, R.G., Muzny, D.M., Nanavati, A.N., Gibbs, R.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NIH-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
Email: cgapbs-fmail.nih.gov
Tissue Procurement: Gilbert Smith, Ph.D.
Tissue Procurement: Gilbert Smith, Ph.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G. B. Consortium (LLNL)
DNA Sequencing by: Baylor College of Medicine Human Genome
                                                                                                                                                                                                                                                                                                                                                                                                                                   . Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
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/mol_type="mRNA"
/strain="FVB/N"
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Query Match:
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                                                       ValArgGlyThrSerAlaAspHisCysValGlnLeuIleAlaAlaGlnGluAlaAspAla
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RSPLEKAVSFFSGSCYPCADPVAFPLCQLCPGCGSSTQFFFGYGAFKCLKDG
GDVAFYRGATIFPGYGAFKCLKDG
GDVAFYRTATIFPGYGAFKCLKDG
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PAEWAKNLKQEDFELLCPDGTRKPVKDFASCHLAQAPNHVVVSRKEKAARVKAVLTSQ
ETLFGGSDCTGNFCLFKSTTKDLLFRDDTKCFVKLPEGTTPEKYLGAEYWQSVGNMRK
Submitted (16-APR-2002) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:genome-res@gsc.riken.go.jp, URL:http://genome.gsc.riken.go.jp/, Tel:81-45-503-9222, Pax:81-45-503-9216)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /tissue type="mammary gland"
/clone_lib="RIKEN full-length enriched mouse cDNA library"
/dev_stage="10 days lactation, adult"
56. _2149
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note="unnamed protein product; putative
transferrin (MGD|MGI:98821, GB|J03299, evidence: BLASTN,
99%, match=393)"
                                                                                                                            cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Rike Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to
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Please visit our web site for further details.
URL:http://genome.gc.riken.go.jp/
URL:http://fantom.gsc.riken.go.jp/.
Location/Qualifiers
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Matches:
Conservative:
Mismatches:
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/mol_type="mRNA"
/strain="C57BL/6J"
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BCO58218 Mus musculus transferrin, mRNA (cDNA clone IMAGE:5388952). BCO58218 BCO58218. GI:37194857 HTC. Mus musculus (house mouse) Mus musculus (bordata, Craniata, Vertebrata, Euteleostomi, Mammalia; Eutheria; Rodentia, Sciurognathi; Muridae, Murinae; Mus.	E. (Dasses 1 to 2332). Strausberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G., Klausner, R.D., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D., Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K., Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Hsieh, F., Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L., Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L., Scheetz, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S., Carninoi, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J., Abramson, R.D., Mullahy, S.J., Bosak, S.A., McEwan, P.J., McKernan, K.J., Malek, J.A., Gunaratne, P.H., Richards, S., Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W., Villalon, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A., Fahey, J., Helton, E., Ketteman, M., Madan, A., Rodriques, S.,	Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shevchenko, Y., Bouffard, G.G., Blakesley, R.W., Toucham, J.W., Green, E.D., Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Wyers, R.M., Butterfield, Y.S., Krzywinski, M.I., Skalska, U., Smailus, D.E., Schmerzh, A., Schein, J.D., Jones, S.J. and Marra, M.A. Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002) 12477932 2 (bases 1 to 2332) 2 (bases 1 to 2332) 2 Krausberg, R. Direct Submission Submitted (15-SEP-2003) National Institutes of Health, Mammalian Submitted (15-SEP-2003) Cancer Genomics Office, National Cancer	USA USA NIH-MGC Project URL: http://mgc.nci.nih.gov Contact: MGC help desk Email: cgapbs-r@mail.nih.gov Tissue Procurement: Lothar Hennighausen Ph.D., Priscilla Furth Ph.D. CDNA Library Preparation: Life Technologies, Inc. CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: National Institutes of Health Intramural Sequencing Center (NISC), Gaithersburg, Maryland; Web site: http://www.nisc.nih.gov/ Contact: nisc mgc@nhgri.nih.gov/ Contact: nisc mgc@nhgri.nih.gov/ Akhter,N:, Ayele,K. Beckgrom-Sternberg,S.M., Benjamin,B., Blakesley,R.W., Boukfard,G.G., Breon,K., Brinkley,C., Blakesley,R.W., Brinklerd,G.G., Breoks,S.,	Hansen, N., Ho.SL., Katlins, E., Kong, P., Latic, P., Legaspi, R., Maduro, Q.L., Masiello, C., Maskeri, B., Mastrian, S.D., McCloskey, J.C., Maduro, Q.L., Masiello, C., Maskeri, B., Mastrian, S.D., McCloskey, J.C., McDowell, J., Pearson, R., Stantripop, S., Thomas, P.J., Touchman, J. W., Tsurgeon, C., Vogt, J.L., Walker, M.B., Wetherby, K.D., Wiggins, L., Young, A., Zhang, LH. and Green, E.D. Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov.scries: IRAK Plate: 127 Row: c Column: 23 This clone has the following problem: no 5' EST match. Location/Qualifiers 12332 /organism="Mus musculus" /mol_type="mRNA" /mol_type="mRNA" /db_xref="taxon:10090"
RESULT 12 BC058218 LOCUS DEFINITION ACCESSION VERSION KEYWORDS SOURCE ORGANISM	REFERENCE AUTHORS	TITLE JOURNAL PUBNED REFERENCE AUTHORS TITLE JOURNAL	REMARK	FEATURES
### ATC	453 ValValAlaValValArgArgAspSerSerHisAlaPheThrLeuAsGGTATTAT 1402 453 ValValAlaValValArgArgAspSerSerHisAlaPheThrLeuAspGluLeuArgGly 472	513 PhephakanalaSerCysvalProValAsnasnProLysAsnTyrProSerSerLeuCys 532	GluLeuargSerGluaspTyrGluLeuCysProAenGlyAlaArgAlaGluValSer AATCTGAAGCAGGAAACTTCGAGTTGCTCTGATGGCACCAGGAAGCCTGGAA GluPheAlaAlaCysAsnLeualaGluIleProProHisAlaValMetValArgProAsp GluPheAlaAlaCysAsnLeualaGluIleProProHisAlaValMetValArgProAsp GluPheAlaAlaCysAsnLeualaGluIleProProHisAlaValMetValArgProAsp GATTTTGCCAGCTGCCACCTGGCCCAAGCTCCAAACCATGTTGTGGTCTCACGAAAAGAG ThrAsnIlePheThrValTyrGlyLeuLeuAspLysAlaGlnAspLeupheGlyAspAspAAGGCAGCCGGGGTTAAAGGCTGTACTGCCAGGAGAAGT HisAsnLysAsnGlyPheLysMetPheAspSerSerAsnTyTHigGGGGAAAGT HisAsnLysAsnGlyPheLysMetPheAspSerSerAsnTyTHisGlyGlnAspLeuLeu HisAsnLysAsnGlyPheLysMetPheAspSerSerAsnTyTHisGlyGlnAspLeuLeu HisAsnLysAsnGlyPheLysMetPheAspSerSerAsnTyTHisGlyGlnAspLeuLeu	PhetysaspalathrvalargalavalprovalGlyGluLysThrTyrArgGlyTrp ::

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                                  model.
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                                  WAP-Tag
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Matches:
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/tissue_type="Wammary tumor. WR
gross tissue."
/clone_lib="NC."
/lab_host="DH10B"
/note="Vector: pCMV-SPORT6"
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ATC-----AGTGAGGGAAAGATAGAGTGTGAGTGAGCAGAGAAGACCACTGAG 1228
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TTGATCTGGGAGATTCTCAAAGTGGCACAGGAACACTTTGGCAAAGGCAAATCAAAAGAC
                                                                                                                                                                  TTTGGGCTGTTAAGGGTCCCCCCAAGGATGACTACAGGCTGTACCTTGGCCATAACTAT
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                 SerGluLeuValProileAlaThrGln---ThrTyrGluAlaTrpLeuGlyHisGluTyr
                                                                                                                                                                                                                                                                                               LeuHisAlaMetLysGlyLeu-----LeuCysAspProAsnArgLeuPro---Pro
                                                                                                                                                                                                                                                                                                                                    TyrLeuArgTrpCysValLeuSerThrProGluIleGlnLysCysGlyAspMetAlaVal
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                                                                   LeuilePheArgLeuLeuAsnGluGlyGlnArgLeuPheSerHis---GluGlySerSer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HisCysMetGluArgileGlnAlaGluGlnValAspAlaValThrLeuSerGlyGluAsp
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	Alignment Scores:	US-10-049-957-4 (1-738) x AY327504 (1-2249) QY	121 TTCCGTGACCACATGAAACCGTCCTTCCAGCTGATGGCCCCCCGGCTTGCCTGT 1	Db 295 GTGGCAGCAGAGTTTATGGATCACTTGAACATCCAGAGCCCACTACTTGGCTGTGGCC 354 Oy 112 ValvalArgArgSerSerHisValThrIleAspThrLeuLysGlyValLysSerCysHis 131	SOB GCCAGTTTCTTCTCGGGCAGTTGTGTCCCCTGTGCAGATCCAGTGGCTTCCCCCAG 185 LeuCysArgLeuCysArgGlyAspSerSerGlyGluGlyValCysAspLysSerProLeu 186 CTGTGTCAACTGTCTCCAGGCTGTGGCTGCTCCCCGACT 205 GluArgTyrTyrAspTyrSerGlyAlaPheArgCysLeuAlaGluGlyAlaGlyAspVal 11
613 GlnPheAlaAlaCysAsnLeuAlaGlnIleProProHisAlaValMetValArgProAsp 63 1826 GATTTTGCCAGGTGCCCCTGGCCCAGACCTCCAACATGTTGTGGTCACGAAAAGAG 18 633 ThrAsnIlePheThrValTyrGlyLeuLeuAspLysAlaGlnAspLeuPheGlyAspAsp 65 1886AAGGCAGCCCGGGTTAAGGCTGTACTGACCAGGAGACTTATTTGGGGGAAGT 19	Oy 653 HisAsnLysAsnGlyPheLysMerPheAspSerSerAsnTyrHisGlyGlnAspLeuLeu 672 Db 1943 GACTGCACCGGCAATTCTTTTTTCAAGTCTACCCAGGACCTTCTG 1993 Oy 673 PheLysAsplaThrValArgAlaValPrOvalGlyGluLysThrThrTyrArgGlyTrp 692	Qy 693 LeuGlyLeuAspTyrValAlaAlaLeuGluGlyMetSerSerGlnGlnCysSerGlyAla 712	AY327504 LOCUS AY327504 LOCUS DEFINITION RALTUS norvegicus liver regeneration-related protein LRRG03 mRNA, COMPLETE Cds. ACCESSION AY37504 AY327504	REFERENCE 1 (bases 1 to 2249) AUTHORS Xu,C.S., Li,W.Q., Li,Y.C., Han,H.P., Wang,G.P., Chai,L.Q., Yuan,J.Y., Yang,K.J., Yan,H.M., Chang,C.F., Zhao,L.F., Ma,H., Wang,L., Wang,S.F., Shi,J.B., Rahman,S., Wang,Q.N. and Zhang,J.B. JOURNAL Unpublished TITLE Liver regeneration after PH Reference AUTHORS Xu,C.S., Li,W.Q., Li,Y.C., Han,H.P., Wang,G.P., Chai,L.Q., Yuan,J.Y., Yang,K.J., Yan,H.M., Chang,C.F., Zhao,L.F., Ma,H., Wang,L., Wang,S.F., Shi,J.B., Rahman,S., Wang,Q.N. and Zhang,J.B. TITLE Submitsion JOURNAL Oliversity, No. 148 Jianshe Road, Xinxiang City, Henan 453002, P.R.	PEATURES Location/Qualifiers 1. 2449 / organism="Rattus norvegicus" / mol type="mcNA" / db_xref="taxon:10116" 1. 2097 / note="x2b; transferrin" / codon_state=1 / produci="liver regeneration-related protein LRRG03" / protein_id="AAP97736.1" / db_xref="id:33187736.1" / db_xref="id:331877746" / kranslation="MRYPAVGALLACAALGLCLAVPDKTVKWCAVSHENTKCISFRDH MKTVLAAGAPRHACVKKTSYQDOITAALGGGARAGHIPLGGAFTPNIKEVAAE FYGSLEHPQTHYLAVAVKKGTPPQLNQLQGGKGSCSPTQPPFGYGAFKCLRDGG GDVAPYKHTTIFEVLPQKADRDQYELGLDNTRKPVDQYEDGYLARIPSHAVVARNGD GKEDLIWEILKVAQEHFGKGKSKOFQLFGSPLGKDLIFKDSAFGLLRVPRRNDYRLYL GHSYYTAIRNQREGYCPEGSIDSAPVKNCALSHQBERAKCDEWSUSSNGQIECESAEST

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bramson, R.D., Mullahy, S.J., Bosak, S.A., McEwan, P.J.,
thale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W.,
illalon, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A.,
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outfard, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D.,
totkenon, M.C., Rodrigues, A.C., Grimwood, J., Schmutz, J., Myers, R.M.,
chnerch, A., Schein, J.E., Jones, S.J. and Marra, M.B.
eneration and initial analysis of more than 15,000 full-length
roc. Natl. Acad. Scl. U.S., 99 (26), 16899-16903 (2002)
ValSerGlnPheAlaAlaCysAsnLeuAlaGlnIleProProHisAlaValMetVal 629
                                                                                                                                                                                                     |||| :::||| |||||| TTTTGGAAAAGGACTGCACTGGCAATTTCTGTTTGTTCCGGTCTTCCACC 1935
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AGGAAGTGTTCAACCTCACGACTCCTAGAAGCCTGCACTTTCCACAAAAGTTAAAAT 2100
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lia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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                                                                                                                                               ProAsp-----ThrAsnIlePheThrValTyrGlyLeuLeuAspLysAlaGlnAsp
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CCTCCATGCC 2172
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                                                                                                     624
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     ValSerAspTyrPheGlyGlySerCysValProGlyAlaGlyGluThrSerTyrSerGlu 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Phe---SerHisGluGlySerSerPheGlnMetPheSerSerGluAlaTyrGlyGlnLys 321
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TTCACCTGGAGCTCTTTGAGAGGCAAGAAGTCCTGCCACACTGCCGTGGACAGGACCGCA
                                                                                              LeuGluArgTyrTyrAspTyrSerGlyAlaPheArgCysLeuAlaGluGlyAlaGlyAsp
                                                                                                                                                                                                                                                                                                                                                                   781 CCGGTGACAGAATACAAGGAGTGCCACCTGGCCCAAGTCCCTTCACATGCTGTGGTATCC
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                                                                                                                                                                                                               ValAlaPheValLy8HisSerThrValLeuGluAsnThrAspGlyLysThrLeuProSer
                                                                                                                                                                                                                                                                               244 TrpGlyGlnAlaLeuLeuSerGlnAspPheGluLeuLeuCysArgAspGlySerArgAla
                                                                                                                                                                                                                                                                                                                                                   264 AspValThrGluTrpArgGlnCysHisLeuAlaArgValProAlaHisAlaValValVal
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                                                                       SerheuCysArgLeuCysArgGlyAspSerSerGlyGluGlyValCysAspLysSerPro
                                                                                                                                                                             625 GAGGAGCCATACTCAGGTTATGCTGGAGCCTTGAGGTGTCTGAGAGACAATGCTGGAGAT
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                                       514 GTATCCAAGTTCTTCTAAAGAGCTGTGTTCCCGGTGCCCAAAAGGATAGATTC---CCC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            98
NIH-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Lochar Hennighausen Ph.D., Robin Humphreys
Tissue Procurement: Lochar Hennighausen Ph.D., Robin Humphreys
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLINL)
DNA Sequencing by: Sequencing Group at the Stanford Human Genome
Center, Stanford University School of Medicine, Stanford, CA 943'
Meb Site: (Dickont, Mark) mcd@paxil.stanford.edu
Contact: (Dickont, Mark) mcd@paxil.stanford.edu
Dickson, M., Schmutz, J., Grimwood, J., Rodriquez, A., and Myers,
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This clone has the following problem: no 5' EST match.
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Conservative:
Mismatches:
Indels:
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/clone lib="NCI CGAP_Mam5"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                 /organism="Mus musculus"
/mol_type="mRNA"
/strain="C57BL/6J"
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/clone="IMAGE:3484893"
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Query Match:
DB:
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Gadachi, J., Alzawa, K., Akimura, T., Arakawa, T., Bono, H., Carninci, P., Bukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hashizume, W. Hayashu, M., Hiranka, T., Hirozane, T., Horzi, F., Inotani, K., Ishii, Y., Itoh, M., Kagawa, T., Kasukawa, T., Katoh, H., Kawai, J., Kojima, Y., Itoh, M., Kagawa, I., Kasukawa, T., Katoh, H., Kawai, J., Kojima, Y., Kondo, S., Konno, H., Kouda, M., Katoh, H., Sawai, T., Miyazaki, R., Murata, M., Nakamura, M., Nahi, K., Nomura, K., Numazaki, R., Ohno, M., Ohsato, N., Sano, H., Sasaki, D., Shibata, K., Shinagawa, A., Takahashi, K., Sakai, T., Takau, T., Takau, M., Muramataki, D., Shibata, K., Shinagawa, A., Takahashi, F., Takau-Akanira, S., Takeda, Y., Tanaka, T., Tomaru, A., Toya, T., Yasunishi, A., Muramatsu, M. and Hayashizaki, Y.

Direct Submission

Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research Group, RIKEN Genome Exploration Research Group, RIKEN Genome Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suchiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:genome-res@gec.riken.go.jp,, Tel:81-45-503-9222, Pax:81-45-503-9216)
                                                  Shibata,K., Itoh,M., Aizawa,K., Nagaoka,S., Sasaki,N., Carninci,P., Konno,H., Akiyama,J., Nishi,K., Kitsunai,T., Tashiro,H., Itoh,M., Sumi,N., Ishii,Y., Nakamura,S., Hazama,M., Nishine,T., Harada,A., Yamamoto,R., Matsumoto,H., Sakaguchi,S., Ikegami,T., Kashiwagi,K., Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E., Watshikagi,K., Yonawa,T., Ozawa,K., Tanaka,T., Matsuura,S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and Hayashizaki,Y. RIKEN integrated sequence analysis (RISA) system-384-format sequencing pipeline with 384 multicapillary sequencer 20530913
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/clone lib="RIKEN full-length enriched mouse cDNA library"
/dev_stage="adult"
j6. 72159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Group Phase I & II Team.
Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs
Nature 420, 563-573 (2002)
6 (bases 1 to 2744)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The FANTOM Consortium and the RIKEN Genome Exploration Research
                                                                                                                                                                                                                                                                                                                                                                                                                       The RIKEN Genome Exploration Research Group Phase II Team and
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Functional annotation of a full-length mouse cDNA collection Nature 409, 685-690 (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note="unnamed protein product; lactotransferrin (MGD|MGI:96837, GB|NM_008522, evidence: BLASIN, 99%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   prepare mouse tissues.
Please visit our web site for further details
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/db_xref="MGI:2400921"
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URL:http://fantom.gsc.riken.go.jp/
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    'organism="Mus musculus"
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/strain="C57BL/6J"
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AK036491 2744 bp mRNA linear HTC 19-SEP-2003 Mus musculus adult male bone cDNA, RIKEN full-length enriched library, clone:9830118019 product:lactotransferrin, full insert
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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High-efficiency full-length cDNA cloning
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/translatorus="WRLLIPELFLEALGICLAKATTVQWCAVSNSEBEEKCLEWQNEM
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